

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2003, 07:22:59 ; Search time 1244 Seconds
(without alignments)

13872.961 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 593
Sequence: 1 cccggtcaccacgctccg.....catcaaaaatgcacagc 593

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

tal number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: gb_om:*
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6: gb_pac:*
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37: em_hg_vrt:*
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39: em_hggo_hum:*
40: em_hggo_mus:*
41: em_hggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332.8	56.1	1203	8	HVU249146
2	302.6	51.0	1062	8	AF035379
3	302.6	51.0	1250	8	AF112150
4	300.4	50.7	1345	6	AR042842
5	300.4	50.7	1345	6	AR095093
6	300.4	50.7	1345	6	AR113350
7	300.4	50.7	1345	6	AR200417
8	300.4	50.7	1345	8	MZEMASD
9	292.2	49.3	1186	8	SB032110
10	283.2	47.8	1289	6	BD012691
11	283.2	47.8	1289	6	BD012691
12	283.2	47.8	1289	23	BD005239
13	281.6	47.5	1347	8	AF345911
14	264.6	44.6	1161	8	AB007504
15	263	44.4	1124	8	AB041020
16	259.8	43.8	1101	8	AF139664
17	258.2	43.5	1196	8	HVU249144
18	258.2	43.5	1196	8	AF058697
19	258.2	43.5	1196	8	AF035378
20	252.4	42.6	1207	8	AF058697
21	201.2	33.4	809	8	AF198175
22	198.2	33.4	942	8	AB050657
23	195	32.9	1032	8	AF305696
24	195	32.9	1070	8	AF306349
25	188.6	31.8	974	8	OS001675
26	188.6	31.8	1031	8	AF091158
27	186.8	31.5	1160	8	BPWADS3GN
28	184.4	31.1	1540	8	HVU249143
29	177.4	29.9	975	8	DC4271147
30	177.4	29.9	998	8	BPWADS4GN
31	175.8	29.6	1085	8	AF305076
32	173.6	29.3	966	8	BPWADS5GN
33	172.6	29.1	1055	8	MDAJ759
34	168.2	28.4	1207	8	AF461740
35	166.8	28.1	914	8	AF139665
36	166.6	28.1	1140	8	PSA279089
37	166.6	28.1	1142	8	BOU67451
38	166.6	28.1	1230	8	MDU78948
39	165.8	28.0	909	8	AY040247
40	165.2	27.9	850	8	GHY9727
41	163.4	27.6	1054	6	AR063254
42	163.4	27.6	1054	6	ATAP1
43	163.4	27.6	1057	6	AR095090
44	163.4	27.6	1057	6	AR200414
45	163.4	27.6	1165	8	AY087956

ALIGNMENTS

RESULT 1
HVU249146
LOCUS HVU249146
DEFINITION Hordeum vulgare mRNA for MADS-box protein 8 (m8 gene).
ACCESSION AJ249146.1 GI:9367312
VERSION
KEYWORDS m8 gene; MADS-box protein 8.
SOURCE Hordeum vulgare subsp. vulgare.
ORGANISM Hordeum vulgare subsp. vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE
Schmitz, J., Franzen, R., Nguyen, T.H., Garcia-Maroto, F., Pozzi, C.,
Salamini, F. and Rohde, W.
1203 bp mRNA linear PLN 14-JUL-2000

TITLE	Cloning, mapping and expression analysis of barley MADS-box genes
JOURNAL	Plant Mol. Biol. 42 (6), 899-913 (2000)
MEDLINE	20346590
PUBMED	10890536
REFERENCE	2 (bases 1 to 1203)
AUTHORS	Schmitz, J.J.
TITLE	Direct Submission
JOURNAL	Submitted (20-AUG-1999) Schmitz J.J., Salamini, Max Planck Institut fuer Zuechtungsforsehung, Carl von Linné Weg 10, 50829 Koeln, GERMANY
FEATURES	
source	location/Qualifiers
	1..1203
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	/cultivar="Atlas"
	/db_xref="taxon:112509"
	/tissue_type="inflorescence"
	/clone_lib="lambda NM1149"
gene	43..873
	/gene="m8"
	43..873
	/gene="m8"
	/codon_start=1
	/product="MADS-box protein 8"
	/protein_id="CAB97354.1"
	/db_xref="gi:9367313"
CDS	
	/translation="MGRKVQLKRIENKINQVTFPSRRNLLKKAHISVLCDAEVA VIVSPKGLIYEVAITDSMDKILIRYERYSTAEKALISAESSEGMWCHERFKIKAKI ETTKCKHLMGEDLDLSLNKEIQLEQLESSLKHISRSHLMSEISLQKERS LOENKALQKELVEROKASRQOOLQOQOQOQOMWBOAQATQTHHTONOPQATSS SSSFPMRMDQAAHPQQNICSPYPMWGEGATTAATAAPEDQAQRLICLPWMLSHLANA "
BASE COUNT	356 a 288 c 308 g 251 t
ORIGIN	
Query Match	56.1%; Score 332.8; DB 8; Length 1203;
Best Local Similarity	96.2%; Pred. No. 2,7e-69;
Matches	352; Conservative 0; Mismatches 12; Indels 2; Gaps 1;
OY	228 CACAAGACCCGACAGCTAGATGCGGAATTCAGAGATGGTGGCGGAGAGTGCACTGA 287
Db	10 CACAGACCGCACACTGATCGTGAATTCGGG--ATGGTGGCGGTTAGGTGCAGCTGA 67
OY	288 AGCGGATGAGAAACAAGATAAATGGCGAGGTGACCTTCCAAAGCGCCGCAACGGGCTCC 347
Db	68 AGCGGATGAGAAACAAGATAAATGGCGAGGTGACCTTCCAAAGCGCCGCAACGGGCTCC 127
OY	348 TGAAGAAAGCGCAGAGATCTCCGCTCTCTGAGACGCGAGAGTCCGCGTCACTCGTCTCT 407
	128 TGAAGAAAGCGCAGAGATCTCCGCTCTCTGAGACGCGAGAGTCCGCGTCACTCGTCTCT 187
OY	408 CCCCCAAAGCAAGCTCTATGAGTACGCGCAGCGACTCCAGCATGAGACAAAATTTCTTGAC 467
Db	188 CCCCCAAAGCAAGCTCTATGAGTACGCGCAGCGACTCCAGCATGAGACAAAATTTCTTGAC 247
OY	468 GTTATGACCGCTACTCTTATAGTGAAGAGCTCTTATTCAGCTGGAATCTGAAGTGAAG 527
Db	248 GTTATGACCGCTACTCTTATAGTGAAGAGCTCTTATTCAGCTGGAATCTGAAGTGAAG 307
OY	528 GAAATTGGTGCCACGAATACAGGAACCTTAAGGCGAAGATTGAGACCATACAAATATGTC 587
Db	308 GGAATTGGTGTCATATAACAGGAACCTTAAGGCGAAGATTGAGACCATACAGAGTGTCTC 367
OY	588 ACAAGC 593
Db	368 ACAAGC 373
RESULT 2	AF035379 1062 bp mRNA linear PLN 29-JAN-1999
LOCUS	Loium temulentum MADS-box protein 2 (MADS2) mRNA, alternatively
DEFINITION	spliced product, complete cds.
ACCESSION	AF035379

VERSION	AF05379.1	GI:4204233
KEYWORDS		
SOURCE	<i>Lolium temulentum</i> .	
ORGANISM	<i>Lolium temulentum</i> . Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Poace; Lolium.	
REFERENCE	Gocal,G.F.W., Blundell,C., Schwartz,O.M. and King,R.W. Expression of Two APETALA1-Related Genes Changes During Inflorescence Initiation of <i>Lolium</i> Unpublished	
JOURNAL	2 (bases 1 to 1062)	
AUTHORS	Gocal,G.F.W., King,R.W. and Blundell,C.	
TITLE	Direct Submission	
JOURNAL	Submitted (20-NOV-1997) PBIO, Salk Institute, 10010 N. Torrey Pines Rd., La Jolla, CA 92037, USA	
FEATURES	Location/Qualifiers	
source	1..1062	
	/organism="Lolium temulentum"	
	/strain="Ceres"	
	/db_xref="taxon:34176"	
	1...1062	
gene	/gene="MADS2"	
	82..867	
CDS	/gene="MADS2"	
	/note="API-related protein; alternatively spliced product"	
	/codon_start=1	
	/product="MADS-box protein 2"	
	/protein_id="AADI0626.1"	
	/db_xref="GI:4204234"	
	/translation="MGRCVOLKRIENKINROYTFSKRNGLKKAHEISVLCAAEVA VVPSFGKIYEVATBDSMPKILERYRYRYAEALISAESSEGMCHREKXAKIKI ETIQCKHLMGEDLECLNRELQQLQLESLSKHTRSKSHLMESISLOKKES ILOENKALEIVEROKAQOQOEODROTOQAQNPOAQTSSSFPMRDQDA HAOONICYPVTVMGEAVAAAPGGCGGLRGIPPMWLISHNA"	
BASE COUNT	316 a	254 c 288 g 204 t
ORIGIN		
Query Match	51.0%; Score 302.6; DB 8; Length 1062;	
Best Local Similarity	94.3%; Pred. No. 4.5e-62;	
Matches 314; Conservative	0; Mismatches 19; Indels 0; Gaps 0;	
Dy	261 ATATGGGTCCGGGAAGTGCAGCTGAACGCCGATAGAACACAATAAATGGCAGCGTA	320
Db	80 AGATGGGTCCGGGAAGTGCAGCTGAACGCCGATAGAACACAATAAATGGCAGCGTA	139
Dy	321 CCTTCCTCAAGCGCGCAAGCGGCTCTCTGAAGAAGCGCACGAGATCTCCGCTCTGTG	380
Db	140 CATTTCTCAAGCGCGCGCAAGCGGCTCTCTGAAGAAGCGCACGAGATCTCCGCTCTGTG	199
Dy	381 ACGCGGAGGTGCGCGTCACTGCTTTCTTCCCCCAAAGGCAAGCTCTTAGTGTAAGCCACCG	440
Db	200 ACGCGGAGGTGCGCGTCACTGCTTTCTTCCCCCAAAGGCAAGCTCTTAGTGTAAGCCACCG	259
Dy	441 ACTCAGCATGGAACAAATTCTTGAAGCTTAGACCGTACTCTTAGCTGAAGAGGCTC	500
Db	260 ACTCAGCATGGAACAAATTCTTGAAGCTTAGACCGTACTCTTAGCTGAAGAGGCTC	319
Dy	501 TTATTTCAGCTGAATCTGAAGTAGAGGAAATTGGTGCACGAATATACAGAACTTAAG	560
Db	320 TGATTTTACGCTGAATCTGAAGTAGAGGAAATTGGTGCATGAATACGAGAACTGAAG	379
Dy	561 CGAAGATTGAGACCATACAAAAATGTCCAAGC	593
Db	380 CGAAGATTGAGACTATACAAAAATGTCCAAGC	412
RESULT 3		
AF112150	AF112150	1250 bp mRNA linear PLN 19-SEP-2001
LOCUS	Zea mays	MADS box protein 3 (mads3) mRNA, complete cds.
DEFINITION		
ACCESSION	AF112150	

VERSION	AF112150.1	GI:12002140
KEYWORDS		
SOURCE	Zea mays.	
ORGANISM	Zea mays.	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.	
AUTHORS	1 (bases 1 to 1250) Heuer, S., Hansen, S., Bantini, J., Bretschneider, R., Kranz, E., Lortz, H., and Dresselhaus, T.	
TITLE	The maize MADS box gene ZmMADS3 affects node number and spikelet development and is co-expressed with ZmMADS1 during flower development, in egg cells, and early embryogenesis	
JOURNAL	Plant Physiol. 127 (1), 33-45 (2001)	
MEDLINE	21437929	
PubMed	11553732	
REFERENCE	2 (bases 1 to 1250) Heuer, S., Dresselhaus, T., and Lortz, H.	
TITLE	Maize MADS box genes expressed in egg cells	
JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 1250) Heuer, S., Dresselhaus, T., and Lortz, H.	
TITLE	Direct Submission	
JOURNAL	Submitted (09-DEC-1998) Centre for Applied Molecular Plant Biology	
FEATURES	AMP II, University of Hamburg, Ohnhorststrasse 18, Hamburg 22609, Germany	
source	Location/Qualifiers	
gene	1..1250 /organism="Zea mays" /strain="A188" /db_xref="taxon:4577" /cell_type="egg" 1..1250 /gene="mads3" /note="expressed in immature male and female flowers, egg cells and nodes" 70..882 /gene="mads3" /codon_start=1 /product="MADS box protein 3" /protein_id="AAG41200.1" /db_xref="GI:12002141" /translation="MGKGVQKRIENKINQVTSKRRNGLLKKAHISVLCDAEVA VIVSPKGLYEYVSDSMKILERYERYSYAEKALISAESSEGNWCEYKLLAKAK EIIORCHHGLMEDELSINPKELOLEQLESSLGHISRSKSLMAESISELOKKE LEENICHLKXELSEROKAVASRQOOQOVOMDQOVONVSSSSPMBOODGGL PPNQCPRPLSISGRGEVAAAQOQLPFGQADQLRIAGLPMLSHLN"	
CDS	361 a 295 c 352 g 242 t	
USE COUNT	361 a 295 c 352 g 242 t	
IGIN		
Query Match	51.0%; Score 302.6; DB 8; Length 1250;	
Best Local Similarity	93.7%; Pred. No. 4,6e-62;	
Matches	314; Conservative 0; Mismatches 21; Indels 0; Gaps 0;	
QY	259 GGATATGGGTCCGGCAAGTGCAGCTGAAGGATAGAGAACAGATAATCCGACAGT 318	
Db	66 GAAATGGGGCGCGCAAGTGCAGCTGAAGGATAGAGAACAGATAAACCGCACAGT 125	
QY	319 GACCTTCCCAAGCGCGCAAGGGCTCTGAAGAAAGCGCAGAGATCTCGTCTCTG 378	
Db	126 GACCTTCCCAAGCGCGCAAGGGCTCTGAAGAAAGCGCAGAGATCTCGTCTCTG 185	
QY	379 TGACGCGGAGGTGCGCGTCAATGTTTCTCCCGCCAAAGCAAGCTCTATGATGACGAC 438	
Db	186 CGACGCCGAGGTCCCGTCAATGTTTCTCCCGCCAAAGCAAGCTCTATGATGACGAC 245	
QY	439 CGACTCGAGTGAACAATTTCTGAACGTTATGAGCGCTACTTATGCTGAAAGGC 498	
Db	246 CGACTCCGAGTGAACAATTTCTGAACGTTATGAGCGCTACTTATGCTGAAAGGC 305	
QY	499 TCTTATTTCACTGAATCTGAAGAGTGAAGGAATTTGTCGCCAGATACAGAAACTTAA 558	
Db	306 TCTTATTTCACTGAATCTGAAGAGTGAAGGAATTTGTCGCCAGATACAGAAACTTAA 365	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AR042842	Sequence 7 from patent US 5811536.	AR042842	AR042842.1	GI:5963338	Unknown.	Unclassified.	1 (bases 1 to 1345)	Yanofsky, M.F.	Caat1: lower floral meristem identity genes and methods of using same
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Best Local Similarity 92.4%; Pred. No. 1.6e-61;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAAATCAGATATGGTCCGGGCAAGGTGACGTGAAGCGGATAGAGAAACAATTAATC 311
DB 138 GCAACAAGGCGATGGGGCGCGCAAGGTACAGCTGAAGCGGATAGAGAAACAATTAATC 197
QY 312 GGCAGGTGACCTTCTCCAAAGCGCGCAAGGGCTCTTGAAGAGGCGACGATCTCCG 371
DB 198 GGCAGGTGACCTTCTCCAAAGCGCGCAAGGGCTCTTGAAGAGGCGACGATCTCCG 257
QY 372 TCCCTGTGACGGGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTCTATAGT 431
DB 258 TCCCTGTGACGGGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTCTATAGT 317
QY 432 ACGCCACCGACTCCAGCATGAGACAAATTTCTTAAGCGCTACTTATGCTG 491
DB 318 ACGCCACCGACTCCAGCATGAGACAAATTTCTTAAGCGCTACTTATGCTG 377
QY 492 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGTCGCAAGTACAGA 551
DB 378 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGTCGCAAGTACAGA 437
QY 552 AACTTAAGCGAAGATTGAGACCATACAAATATGTCAACG 593
DB 438 AACTGAAGCGCAAAATTTGAGACCATACAAATATGTCAACG 479

RESULT 6
AR11350 1345 bp DNA linear PAT 14-FEB-2001
LOCUS AR11350
DEFINITION Sequence 7 from patent US 6127123.
ACCESSION AR11350
VERSION AR11350.1 GI:12828198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1345)
AUTHORS Yanofsky, M.F.
TITLE Cauliflower floral meristem identity genes and methods of using same
JOURNAL Patent: US 6127123-A 7 03-OCT-2000;
ATTORNEYS Location/Qualifiers
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source /organism="unknown"

BASE COUNT 349 a 373 c 358 g 265 t
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Query Match 50.7%; Score 300.4; DB 6; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.6e-61;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAAATCAGATATGGTCCGGGCAAGGTGACGTGAAGCGGATAGAGAAACAATTAATC 311
DB 138 GCAACAAGGCGATGGGGCGCGCAAGGTACAGCTGAAGCGGATAGAGAAACAATTAATC 197
QY 312 GGCAGGTGACCTTCTCCAAAGCGCGCAAGGGCTCTTGAAGAGGCGACGATCTCCG 371
DB 198 GGCAGGTGACCTTCTCCAAAGCGCGCAAGGGCTCTTGAAGAGGCGACGATCTCCG 257
QY 372 TCCCTGTGACGGGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTCTATAGT 431
DB 258 TCCCTGTGACGGGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTCTATAGT 317
QY 432 ACGCCACCGACTCCAGCATGAGACAAATTTCTTAAGCGCTACTTATGCTG 491
DB 318 ACGCCACCGACTCCAGCATGAGACAAATTTCTTAAGCGCTACTTATGCTG 377

QY 492 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGTCGCAAGTACAGA 551
DB 378 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGTCGCAAGTACAGA 437
QY 552 AACTTAAGCGAAGATTGAGACCATACAAATATGTCAACG 593
DB 438 AACTGAAGCGCAAAATTTGAGACCATACAAATATGTCAACG 479

RESULT 7
AR200417 1345 bp DNA linear PAT 20-APR-2002
LOCUS AR200417
DEFINITION Sequence 7 from patent US 6355863.
ACCESSION AR200417
VERSION AR200417.1 GI:20250491
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1345)
AUTHORS Yanofsky, M.F.
TITLE Seed plants exhibiting inducible early reproductive development and methods of making same
JOURNAL Patent: US 6355863-A 7 12-MAR-2002;
ATTORNEYS Location/Qualifiers
1. 1345
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ORIGIN

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Best Local Similarity 92.4%; Pred. No. 1.6e-61;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAAATCAGATATGGTCCGGGCAAGGTGACGTGAAGCGGATAGAGAAACAATTAATC 311
DB 138 GCAACAAGGCGATGGGGCGCGCAAGGTACAGCTGAAGCGGATAGAGAAACAATTAATC 197
QY 312 GGCAGGTGACCTTCTCCAAAGCGCGCAAGGGCTCTTGAAGAGGCGACGATCTCCG 371
DB 198 GGCAGGTGACCTTCTCCAAAGCGCGCAAGGGCTCTTGAAGAGGCGACGATCTCCG 257
QY 372 TCCCTGTGACGGGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTCTATAGT 431
DB 258 TCCCTGTGACGGGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTCTATAGT 317
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DB 318 ACGCCACCGACTCCAGCATGAGACAAATTTCTTAAGCGCTACTTATGCTG 377
QY 492 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGTCGCAAGTACAGA 551
DB 378 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGTCGCAAGTACAGA 437
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DB 438 AACTGAAGCGCAAAATTTGAGACCATACAAATATGTCAACG 479

RESULT 8
MZEMADSD 1345 bp mRNA linear PIN 16-MAY-1996
LOCUS MZEMADSD
DEFINITION Zea mays MADS-box protein (ZAP1) mRNA, complete cds.
ACCESSION L46400
VERSION L46400.1 GI:939784
KEYWORDS MADS box protein.
SOURCE Zea mays cDNA to mRNA.
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 1345)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.

AUTHORS Mena, M., Mandel, M.A., Lerner, D.R., Yanofsky, M.F. and Schmidt, R.J.
 TITLE A characterization of the MADS-box gene family in maize
 JOURNAL Plant J. 8 (6), 845-854 (1995)
 MEDLINE 96132144
 PUBMED 8580958

FEATURES
 source location/Qualifiers

1. .1345
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BASE COUNT 349 a 358 g 265 t
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 Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAATCAGATATGCTCGCGCAAGTGCAGCTGAAGCGGATAGAAACAATTAATC 311
 DB 138 GCACACAGCGAGTGGGCGCGGCAAGTACCTGAAGCGATAGAACACATTAACC 197
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 DB 198 GCGAGGTGACCTTCTCCAAAGCGCGGAAAGCGCTCTGAAGAGCGCAAGATCTCG 257
 QY 372 TCCTCTGACGCGGAGTCCGCTCATGCTCTTCTCCCAAGCGCAAGCTTATGAGT 431
 DB 258 TCCTCTGACGCGGAGTCCGCTCATGCTCTTCTCCCAAGCGCGCAAGCTTATGAGT 317
 QY 432 AGCCACGCACTCCAGCATGACAAATCTTGAAGCTTATGAGCGCTATGCTG 491
 DB 318 AGCCACGCACTCCAGCATGACAAATCTTGAAGCTTATGAGCGCTATGCTG 377
 QY 492 AAAAGGCTTATTTCAGTGAATCTGAAGTGAAGAAATGGTCCAGATACAGA 551
 DB 378 AAAAGGCTTATTTCAGTGAATCTGAAGTGAAGAAATGGTCCAGATACAGA 437
 QY 552 AACTTAAGCGGAAGATTGAGCATACAAAATGTCTACAAGC 593
 DB 438 AACTGAAGGCCAAATTAAGACCCATCAAAAATGACACAGC 479

RESULT 9
 SBUS2110 1186 bp mRNA linear PLN 24-MAR-1997
 LOCUS Sorghum bicolor putative MADS box protein (SBMADS2) mRNA, partial
 DEFINITION cds.
 ACCESSION U32110.1 GI:1905933
 VERSION U32110.1
 KEYWORDS Sorghum bicolor.
 SOURCE Sorghum bicolor.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogonae; Sorghum.
 REFERENCE 1 (bases 1 to 1186)
 Greco, R., Stagi, L., Colombo, L., Angenent, G.C., Sari-Gorla, M. and
 Pe, M.E.

TITLE MADS box genes expressed in developing inflorescences of rice and
 sorghum
 JOURNAL Mol. Genet. 253 (5), 615-623 (1997)
 MEDLINE 97218034
 PUBMED 9065695

REFERENCE 2 (bases 1 to 1186)
 Greco, R., Stagi, L., Colombo, L., Pe, M.E. and Angenent, G.C.
 Direct Submission
 JOURNAL Submitted (21-JUN-1995) Raffaella Greco, Universita' di Milano,
 Genetica e Biologia dei Microorganismi, Via Celoria 26, Milano, MI,
 Italia, 20133

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 source location/Qualifiers

1. .1186
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 QY 393 CCGTATGCTTCTCCCAAGGCAAGCTTATGAGTACGCCAGCTCCGATG 452
 DB 121 CCGTATGCTTCTCCCAAGGCAAGCTTATGAGTACGCCAGCTCCGATG 180
 QY 453 ACAAAATCTTGAAGCTTATGAGCGCTACTCTATGTAAGAGCTCTTATTTCAGCTG 512
 DB 181 ACAAAATCTTGAAGCTTATGAGCGCTACTCTATGTAAGAGCTCTTATTTCAGCTG 240
 QY 513 AATCTGAAGTGAAGAAATGGTCCACGAATACAGAAAATTAAAGCGAAGATTGAGA 572
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 QY 573 CCATACAAAATGTCTACAAGC 593
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RESULT 10
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 DEFINITION AF058698
 ACCESSION AF058698
 VERSION AF058698.1
 KEYWORDS Oryza sativa.
 SOURCE Oryza sativa.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

TITLE Characterization of rice MADS box-like genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1289)
AUTHORS Sasaki, T.
TITLE Direct Submission
SUBMITTED (23-APR-1997) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@abr.affrc.go.jp, Tel: 0298-38-7441,
Fax: 0298-38-7468)

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BASE COUNT 354 a 316 c 337 g 282 t
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Matches 306; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 250 GCGAATTCAGATATGCGTCGCGCAAGTGCCTGAAAGCGATAGAGAACAGATAA 309
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DB 172 CAGGCGAGTGACCTTCCAGAGCGCGCAAGCGGCTCCGGAAGAGCGCAGAGATCTC 231
QY 370 CGTCTCTGTGACGCGGAGGTGCGCGCATGCTCTTCTCCCAAGGCAAGCTCTATGA 429
DB 232 CGTCTCTGTGACGCGGAGGTGCGCGCATGCTCTTCTCCCAAGGCAAGCTCTATGA 291
QY 430 GTACGCCACGACTCCAGATGAGCAAAATCTTGAAGCTATAGCGCTACTCTTATGC 489
DB 292 GTACGCCACGACTCCAGATGAGCAAAATCTTGAAGCTATAGCGCTACTCTTATGC 351
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QY 550 GAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCAACAAC 593
DB 412 GAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCAACAAC 455

RESULT 13
BD005239 standard; DNA; PLN; 1289 BP.
ID BD005239
XX BD005239;
SV BD005239.1

DT 08-FEB-2002 (Rel. 70, Created)
DT 08-FEB-2002 (Rel. 70, Last updated, Version 1)
XX A gene controlling for branching of plants, a vector containing said gene,
DE an microorganism containing said vector and a method for controlling of

DE branch of plant.
XX JP 03075374-T/1.
XX
XX Oryza sativa
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae;
OC Oryzae; Oryza.

RP 1-1289
RA Kojima M., Sasaki T., Nozue M., Shioiri H.;
RT "A gene controlling for branching of plants, a vector containing said gene,
RT an microorganism containing said vector and a method for controlling of
branch of plant";
RL Patent number JP03075374-T/1, 16-FEB-2001.
RL KUMARI CHEMICAL INDUSTRY CO LTD, MINO KOJIMA, TAKUJI SASAKI, ASAYUKI NOZUE,
RL HIDEHARI SHIOIRI.

OS Oryza sativa (rice)
CC PN JP 03075374-T/1
CC PD 16-FEB-2001
CC PF 18-AUG-2000 JP 200005537
CC PR 19-AUG-1999 JP 99P 232318
CC PI MINO KOJIMA, TAKUJI SASAKI, MASAYUKI NOZUE, HIDEHARI SHIOIRI
CC PC C12N15/29, A01H5/00
CC CC
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CC FT source 1..1289
CC FT /organism="Oryza sativa (rice)"

Key Location/Qualifiers
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FH /organism="Oryza sativa"
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Query Match 47.8%; Score 283.2; DB 23; Length 1289;
Best Local Similarity 89.0%; Pred. No. 2,1e-57;
Matches 306; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 250 GCGAATTCAGATATGCGTCGCGCAAGTGCCTGAAAGCGATAGAGAACAGATAA 309
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QY 310 TCGGCGAGTGACCTTCCAGAGCGCGCAAGCGGCTCCGGAAGAGCGCAGAGATCTC 369
DB 172 CAGGCGAGTGACCTTCCAGAGCGCGCAAGCGGCTCCGGAAGAGCGCAGAGATCTC 231
QY 370 CGTCTCTGTGACGCGGAGGTGCGCGCATGCTCTTCTCCCAAGGCAAGCTCTATGA 429
DB 232 CGTCTCTGTGACGCGGAGGTGCGCGCATGCTCTTCTCCCAAGGCAAGCTCTATGA 291
QY 430 GTACGCCACGACTCCAGATGAGCAAAATCTTGAAGCTATAGCGCTACTCTTATGC 489
DB 292 GTACGCCACGACTCCAGATGAGCAAAATCTTGAAGCTATAGCGCTACTCTTATGC 351
QY 499 TGAAGAAGCTCTTATTTAGCTGTAATCTGAAGTGAAGGAAATGGTGCACGATACAG 549
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DB 412 GAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCAACAAC 455

RESULT 14
AF345911 1347 bp mRNA linear PLN 02-OCT-2001
LOCUS AF345911
DEFINITION Oryza sativa MADS-box protein FDRMADS3 mRNA, complete cds.
ACCESSION AF345911

VERSION AF345911.1 GI:15824794
 KEYWORDS
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhacoidae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 1347)
 AUTHORS Gao, Z., Chen, R., Jia, H. and Sun, C.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-2001) Biochemistry, Fudan University, 220 Handan Road, Shanghai 200433, P.R. China
 FEATURES
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 Oy 550 GAAACTTAAGCGAGATGAGACCATACAAAATGTCAACAGC 593
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 DEFINITION complete cds.
 ACCESSION AB007504
 VERSION AB007504.1 GI:3688588
 KEYWORDS TAMADS#11; MADS box transcription factor.
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 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poaceae; Triticeae; Triticum.
 REFERENCE 1
 AUTHORS Murai, K., Murai, R., Takumi, S. and Ogihara, Y.

TITLE Cloning and characterization of cDNAs corresponding to the wheat
 MADS box genes
 JOURNAL (in) A.E. Slinkard (Ed.):
 PROCEEDINGS OF THE 9TH INTERNATIONAL WHEAT GENETICS SYMPOSIUM:
 89-94;
 REFERENCE 2
 AUTHORS Murai, K., Murai, R., Takumi, S. and Ogihara, Y.
 TITLE CDNA cloning of three MADS box genes in wheat (Accession Nos.
 JOURNAL AB007504, AB007505 and AB007506) (PGR98-159)
 JOURNAL Plant Physiol. 118, 330 (1998)
 REFERENCE 3
 AUTHORS Murai, K., Takumi, S., Koga, H. and Ogihara, Y.
 TITLE Pteriloddy, homeotic transformation of stamens into pistil-like
 structures, caused by nuclear-cytoplasm interaction in wheat
 JOURNAL Plant U. 29 (2), 169-181 (2002)
 MEDLINE 21841579
 PUBMED 11851918
 REFERENCE 4 (bases 1 to 1161)
 AUTHORS Murai, K.
 TITLE Direct Submission
 JOURNAL Submitted (22-SEP-1997) Koji Murai, Fuku Prefectural University,
 Department of Bioscience; 4-1-1, Kenjo-jiima, Matsuo-cho,
 Yoshida-gun, Fukuji 910-1195, Japan (E-mail: murai@fpu.ac.jp,
 Tel: 0776-61-6000 (ex. 3618), Fax: 0776-61-6015)
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OY 559 GCGGAAGATTGAGACCATACAAAAATGTCACAGC 593
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

tal number of hits satisfying chosen parameters: 4370478

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES.

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4	300.4	50.7	1345	19	AAV58307
5	300.4	50.7	1345	19	AAV86631
6	300.4	50.7	1345	19	AAV02763
7	300.4	50.7	1345	19	AAV06021
8	300.4	50.7	1345	21	AAC61410
9	300.4	50.7	1345	21	AAZ57057

10	300.4	50.7	1345	21	AAZ92144
11	283.2	47.8	1289	22	AAAF75749
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15	189.4	31.9	1305	21	AAAC44058
16	177.4	29.9	1084	17	AAT34429
17	174.2	29.4	1223	21	AAAC55901
18	164.6	27.8	738	22	AAAC90635
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21	163.4	27.6	1057	19	AAV06018
22	163.4	27.6	1057	21	AAZ57054
23	163.4	27.6	1057	21	AAZ92141
24	163.4	27.6	1163	21	AAAC51102
25	163.4	27.6	1165	21	AAAC37677
26	163.4	27.6	1215	18	AAAT76885
27	163.4	27.6	1215	19	AAV58306
28	163.4	27.6	1215	21	AAAC61407
29	163.4	27.6	1220	21	AAAI5016
30	160.2	27.0	1239	21	AAZ49161
31	158.6	26.7	794	18	AAAT76886
32	158.6	26.7	794	19	AAV58316
33	158.6	26.7	794	19	AAAT86629
34	158.6	26.7	794	19	AAV02761
35	158.6	26.7	794	21	AAV06019
36	158.6	26.7	794	21	AAAC61408
37	158.6	26.7	794	21	AAZ57055
38	158.6	26.7	794	21	AAZ92142
39	158.4	26.7	1062	20	AAV18594
40	158.4	26.7	1062	20	AAV98856
41	158.4	26.7	1123	21	AAC41877
42	156.6	26.4	768	18	AAAT76887
43	156.6	26.4	768	19	AAV58317
44	156.6	26.4	768	19	AAAT86630
45	156.6	26.4	768	19	AAV02762

ALIGNMENTS

RESULT 1	
ID	AAAC3733 standard; DNA; 496 BP.
AC	AAAC3733;
ID	18-OCT-2000 (first entry)
DE	Zea mays DNA fragment SEQ ID NO: 40312.
XX	
KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway; metabolic;
KW	pathway; promoter; termination sequence; corn; ss.
XX	
OS	Zea mays subsp. mays.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.

Corn APETALAI (API)
Rice MADS box gene
Zea mays DNA fragm
Eucalyptus SOE25 C
Eucalyptus SOE2L C
Zea mays DNA fragm
Eucalyptus SOE1 CD
Eucalyptus grandis
Strawberry flower1
APETALAI gene from
Arabidopsis floral
Arabidopsis floral
A. thaliana API pr
APETALAI (API) nuc
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
CDNA encoding a Ap
CDNA encoding the
MADS box gene. Ge
Brassica oleracea
Brassica oleracea
Brassica oleracea
APETALAI gene from
Brassica oleracea
Brassica floral me
CDNA encoding a Ap
B. oleracea API pr
Brassica oleracea
Arabidopsis AGI n
Arabidopsis AGI-1
Arabidopsis thalia
Calliflower floral
Brassica oleracea
APETALAI gene from
Calliflowera flora

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130649.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0133248.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
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PR 06-JUL-1999; 99US-0142390.
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PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144335.
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PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
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PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
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PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148341.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.

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PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 51.0%; Score 302.6; DB 21; Length 496;
Best Local Similarity 93.7%; Pred. No. 5.3e-76;
Matches 314; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 259 GGAATATGGTCCGCGGCAAGTGCAGTGAAGCGATAGAAACAAGATAATCGCAGGT 318
DB 65 GAAGATGGGCGCGGCAAGTGCAGTGAAGCGATAGAAACAAGATAATCGCAGGT 124
QY 319 GACCTTCTCCAGCGCGGCAAGTGCAGTGAAGCGGCTCTGAAGAGCGGCAAGATCTCGTCTTG 378
DB 125 GACCTTCTCCAGCGCGGCAAGTGCAGTGAAGAGCGGCAAGATCTCGTCTTG 184
QY 379 TGACCGGAGGTCCGCGTCAATGCTTTCTCCCAAGGCAAGCTCTATGATAGCGCAC 438
DB 185 CGACGCGGAGGTCCGCGTCAATGCTTTCTCCCAAGGCAAGCTCTATGATAGCGCAC 244
QY 439 CGACTTCAGCATGACAAATTTCTGAAGCGTATGAGCGCTACTTATGCTGAAGGCG 498
DB 245 CGACTTCAGCATGACAAATTTCTGAAGCGTATGAGCGCTACTTATGCTGAAGGCG 304
QY 499 TCTTATTTCACTGAATCTGAAGTGAAGGCAATGCTCCCAAGATACAGAACTTAA 558
DB 305 TCTTATTTCACTGAATCTGAAGTGAAGGCAATGCTCCCAAGATACAGAACTTAA 364
QY 559 GCGGAGATTGAGACCATACAAATTTCTGACAAAGC 593
DB 365 GCGGAGATTGAGACCATACAAATTTCTGACAAAGC 399

RESULT 2
AAF85192
ID AAF85192 standard; cDNA; 1250 BP.

AC AAF85192;
DT 09-JUN-2001 (first entry)

DE Nucleotide sequence of a maize ZmMAD3 protein.

KM MAD3; flower development; flower structure; seed development;
KM fruit development; transgenic plant; ss.

OS Zea mays.

XX Key Location/Qualifiers
FH 70..882
FT CDS /tag= a
FT /product= "ZmMAD3"

XX WO200131017-A2.
PN 03-MAY-2001.
XX 25-OCT-2000; 2000MO-EP10484.
XX 25-OCT-1999; 99EP-0120842.
XX (SUSD-) SUEDEWESTDEUTSCHE SAATZUCHT.
XX Dresselhaus T, Heuer S, Loez H;
XX WPI; 2001-31635/33.
DR P-PSDB; AAB68357.
XX New polynucleotide encoding ZmMAD3 protein, for use in cloning and
PT expression in plant a nucleic acid sequence encoding protein
PT influencing flower structure, function and/or its seed and/or fruit
PT development

PS Claim 1; Page 67; 71pp; English.

CC The present sequence encodes a maize MAD3 protein, designated ZmMAD3.
CC The ZmMAD3 protein is essential for flower development and is active
CC in flowers, in particular, in immature flowers and female flowers,
CC but also in the mature embryo sac of maize. The ZmMAD3 protein is also
CC active in nodes and adjacent cell layers. ZmMAD3 polynucleotides and
CC polypeptides are useful influencing flower structure, function and
CC seed or fruit development in transgenic plants.

Sequence 1250 BP; 361 A; 295 C; 352 G; 242 T; 0 other;

Query Match 51.0%; Score 302.6; DB 22; Length 1250;
Best Local Similarity 93.7%; Pred. No. 7.7e-76;
Matches 314; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 259 GGAATATGGTCCGCGGCAAGTGCAGTGAAGCGGATAGAAACAAGATAATCGCAGGT 318
DB 66 GAAGATGGGCGCGGCAAGTGCAGTGAAGCGGATAGAAACAAGATAATCGCAGGT 125
QY 319 GACCTTCTCCAGCGCGGCAAGTGCAGTGAAGCGGCTCTGAAGAGCGGCAAGATCTCGTCTTG 378
DB 126 GACCTTCTCCAGCGCGGCAAGTGCAGTGAAGAGCGGCAAGATCTCGTCTTG 185
QY 379 TGACCGGAGGTCCGCGTCAATGCTTTCTCCCAAGGCAAGCTCTATGATAGCGCAC 438
DB 186 CGACGCGGAGGTCCGCGTCAATGCTTTCTCCCAAGGCAAGCTCTATGATAGCGCAC 245
QY 439 CGACTTCAGCATGACAAATTTCTGAAGCGTATGAGCGCTACTTATGCTGAAGGCG 498
DB 246 CGACTTCAGCATGACAAATTTCTGAAGCGTATGAGCGCTACTTATGCTGAAGGCG 305
QY 499 TCTTATTTCACTGAATCTGAAGTGAAGGCAATGCTCCCAAGATACAGAACTTAA 558
DB 306 TCTTATTTCACTGAATCTGAAGTGAAGGCAATGCTCCCAAGATACAGAACTTAA 365
QY 559 GCGGAGATTGAGACCATACAAATTTCTGACAAAGC 593
DB 366 GCGGAGATTGAGACCATACAAATTTCTGACAAAGC 400

RESULT 3
AAT99437
ID AAT99437 standard; cDNA; 1342 BP.

AC AAT99437;
DT 11-MAY-1998 (first entry)

DE Maize floral meristem identity gene APETALA (AP1 or ZAP-1) cDNA.

XX Floral meristem identity gene; APETALA1, AP1 gene; maize; ZAP-1;

KW flower development; transgenic plant; angiosperm; ss.

Zea mays.

	Key	Location/Qualifiers
FH	CDS	149..970
FT		
FE		

PN WO9727287-A1.

PD 31-JUL-1997

PF 26-JAN-1996; 96WO-US01041.

PR 26-JAN-1996; 96WO-US01041.

PA (REGC) UNIV CALIFORNIA.

PI Yanofsky MF;

WPI; 1997-393675/36.

33 XX

PT Cauliflower floral meristem identity genes and related proteins
PT used to develop products for converting shoot meristem to floral
PT meristem and promoting early flowering in an angiosperm

PS Example 1; Fig 4A-B; 132pp; English

CC This sequence comprises maize ZAP-1 cDNA, that encodes a floral
CC meristem identity gene product (see AN233814) that is involved in the
CC conversion of shoot meristem to floral meristem. The clone was
CC isolated from a Zea mays ear cDNA library using Arabidopsis AP1
CC cDNA (see AAT76885) as probe. Sequence homology indicates that
CC ZAP-1 is the maize orthologue of Arabidopsis APETALA-1 (AP1).
CC Mutation of an AP1 gene results in replacement of a few basal
CC flowers by inflorescence shoots that are not subtended by flowers.
CC When AP1 is ecotypically expressed in shoot meristem, the shoot
CC meristem is converted to floral meristem and early flowering can
CC occur. The invention relates to floral meristem identity genes
CC AP1, LFY and especially CAL (see AAT76885-97 and AAT99417) and their
CC use in converting shoot meristem to floral meristem and in
CC promoting early flowering in transgenic plants, especially
CC angiosperms such as cereal plants, leguminous plants, oilseed
CC plants, trees, fruit-bearing plants and ornamental flowers.

SQ Sequence 1342 BP; 347 A; 373 C; 358 G; 264 T; 0 other;

Query Match	Score	DB	Length
50.78;	300.4;	18;	1342;

Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0.

252 GAAATCAGGATATGGGTCGGCGAAGGTGCAGCTGAAGCGGATAGAGAACAGATAATC 311

OY	252	GAATACAGGATATATGGGTCCGCGCAAGGTGCACTGAAAGCGATAGGAACAAGATAATCT	311
Db	138	GCAACAAGGCCATGGGGCGCGCAAGGTACAGGTGAAGCGATAGGAACAAGATAAAC	197
OY	312	GCGAGGTGACTTTCTTCCAAAGCGCGCAACGGGCTCTTAAGAAAGCGCACAGATCTCCG	371
Db	198	GCGAAGTGACTTTCTTCCAAAGCGCGGAAAGGCGCTGTCTAAGAAAGGCGACGAGATCTCCG	257
OY	372	TCCTCTGTGACCGCGAGGTGCGCGTATCGTCTTCTTCCCAAGGCAAGCTCTATAGT	431
Db	258	TCCTCTGCGATGCCAAGGTGCGCGTATGTTCTTCTCCCAAGGCAAGCTCTACGAT	317
OY	432	ACGCCACCGACTTCACGATGGAACAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTG	491
Db	318	ACGCCACCGACTTCGCCATGGAACAATTTCTTGAAGCGCTATGAGCATTTTCTTATGCGG	377
OY	492	AAAAGGCTTTATTTTACGCTGAATCTGAAAGTAGAGGAATTTGTTCCACGAATACAGA	551
Db	378	AAAAGGCTTTATTTTACGCTGAATCTGAAAGTAGAGGAATTTGTTCCACGAATACAGA	437
OY	552	AACCTTAAGCGGAAGATTGAGACCATACAAAATATGTCACAGC	593

Db 438 AACTGAAGGCCAAATTTGAGACCATACAAATAATGCCACAAGC 479

RESULT 4
AAV58307
ID AAV58307 standard; DNA; 1345 BP.

AC AAV58307

DT 19-NOV-1998 (first entry)

DE Zea mays AP1 gene.

KW CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;

XX

XX

FT	CDS	149..970
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XXXX

XXXX

XX

XX
XX

[illegible]XX
XX
XX

XX 1000 F200AF/AF
25

DR : P-PSDB; AAJW69328.

cloned CAULIFLOWER genes - and vectors for converting snoot

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XX This sequence encodes the Zea mays APl protein (ZAp1). This sequence
CC was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER
CC (CAL) protein of the invention. An expression vector containing the CAL
CC DNA sequence can be used to convert shoot meristems to floral meristems
CC, especially to promote early flowering in angiosperms.

SQ Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 19; Length 1345;

Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

252 GAAATCAGGATATGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGACAAGATAATC 311

QY	252	GAATTCAGGATATGGTTCGCGCGCAAGGTCAGCTGAAGCGGATGAGAAACAAGTAAATC	311
Db	138	GCAACAAGCGCATGGGGGCGCGCAAGGTACAGCTGAAGCGGATGAGAAACAAGTTAAAC	197
QY	312	GGCAGTGACCTTCTCCCAAGCGCGCAACGGGCTCCTGAABAAGCGCAGCAGATCTCCG	371
Db	198	GGCAGGTACCTTCTCCCAAGCGCGGAACGGCTGCTCAGAAAGCGCACAGATCTCCG	257
QY	372	TCTCTGTGACGCGAAGGTGCGCGCTCATGCTTCTCTCCCAAGGCAAGCTCTATGAGT	431
Db	258	TCTCTGTGATGCGGAGGTTCGCGCTCATGCTTCTCTCCCAAGGCGAAGTCTTACGAGT	317
QY	432	AAGCACCAGATCTCCAGCATGAGCAAAATCTTGAACGTTATGAGCGCTACTCTTATGCTG	491
Db	318	AAGCACCAGATCTCCGATGAGCAAAATCTTGAACGTTATGAGGATATTTCTATGCTG	377
QY	492	AAAAAGCTTATTTCACTGAAATCTGAABAATGAGGGAATTTGGGCCACGAATTCAGGA	551

DB 378 AAAAGGCTTTATTTTCAGCTGAATCTGAAAGTGAGGAAATTGGTCCACGAATACAGA 437
 QY 552 AACTTAAGCGGAAGATTGAGACCATACAAAATGTCCAAAGC 593
 DB 438 AACTGAAGGCCAAATTTGAGACCATACAAAATGTCCAAAGC 479

RESULT 5
 AAT86631
 ID AAT86631 standard; DNA; 1345 BP.
 XX

AC AAT86631;

DT 18-JUN-1998 (first entry)

DE APETALA1 gene from Zea mays.

XX Transgenic plant; ectopically expressed; meristem gene; APETALA1;
 KM API; CAULIFLOWER; CAL; LEAFY; LFY; reproductive development;
 angiosperm; ds.

XX Zea mays.

XX Key Location/Qualifiers
 FH CDS 149..970
 FT /*tag= a
 FT /product= API_gene_product

PN W09746077-A1.

PD 11-DEC-1997.

PF 05-JUN-1996; 96WO-US09429.

PR 05-JUN-1996; 96WO-US09429.

PA (REGC) UNIV CALIFORNIA.

PI Weigel D, Yanofsky MF;

DR MPI: 1998-041769/04.
 P-PSDB; AAW43112.

XX Transgenic plant comprising an ectopically expressed floral meristem
 PT gene - for promoting early reproductive development and controlling
 PT the time of seed-derived crop harvest(s) in e.g. grapes, beans,
 PT corn, wheat, etc

XX Example 5; Pages 125-127; 158pp; English.

XX The present sequence encodes a floral meristem identity gene product,
 CC APETALA1 (API), from Zea mays. The invention relates to a non-naturally
 CC occurring seed plant comprising a first ectopically expressible nucleic
 CC acid encoding a first floral meristem identity gene product, provided
 CC that the first nucleic acid is not ectopically expressed due to a
 CC mutation in an endogenous TERMINAL FLOWER gene. The invention describes
 CC a method of converting shoot meristem to floral meristem, especially in
 CC order to promote early reproductive development, in an angiosperm, which
 CC comprises introducing a first ectopically expressible nucleic acid
 CC molecule encoding a first floral meristem identity gene product into the
 CC angiosperm. Ectopic expression of the floral meristem gene product in
 CC the shoot meristem tissue of the transgenic plant, allows selection of
 CC the line of seed development in the plant which can be useful for
 CC manipulating the time of crop harvest in seed-derived crops such as
 CC grapes, beans, corn, wheat, rice, hop, etc., or to hasten the breeding
 CC of e.g. tree species, for insect or disease resistance.

XX Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

XX Query Match 50.7%; Score 300.4; DB 19; Length 1345;
 XX Best Local Similarity 92.4%; Pred. No. 3.3e-75;
 XX Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAAATCAGAGATATGGGTGCGCGCAAGTGACGCTGAAACGGATAGAGACAAAGATTAATC 311
 DB 138 GCAACAGAGCGATGGGCGCGGCAAGGTATACAGCTGAACGGATAGAGACAAAGATTAAC 197
 QY 312 GGCAGGTGACCTTCTTCCAGAGCGCGCAACGGGCTCTTGAAGAGCGGACGATCTCG 371
 DB 198 GGCAGGTGACCTTCTTCCAGAGCGCGGAAACGGGCTCTTGAAGAGCGGACGATCTCG 257
 QY 372 TCCTCTGTGACGCGGAGGTGCGCGCATGCTTCTTCCCGCAAGGACGCTTATGAGT 431
 DB 258 TCCTCTGTGATGCGAGGTGCGCGCATGCTTCTTCCCGCAAGGACGATCTTATGAGT 317
 QY 432 ACGCACCGACGCTCCAGCATGAGCAAAAATTTCTTGAAGCTTATGAGCGCTTATGCTG 491
 DB 318 ACGCACCGACGCTCCGCGATGAGCAAAAATTTCTTGAAGCGCTTATGAGCGATATCTGCTG 377
 QY 492 AAAAGGCTTTATTTTCAGCTGAATCTGAAAGTGAGGAAATTGGTCCACGAATACAGA 551
 DB 378 AAAAGGCTTTATTTTCAGCTGAATCTGAAAGTGAGGAAATTGGTCCACGAATACAGA 437
 QY 552 AACTTAAGCGGAAGATTGAGACCATACAAAATGTCCAAAGC 593
 DB 438 AACTGAAGGCCAAATTTGAGACCATACAAAATGTCCAAAGC 479

RESULT 6
 AAV02763
 ID AAV02763 standard; cDNA; 1345 BP.

XX AAV02763;

DT 08-JUN-1998 (first entry)

DE Maize floral meristem identity gene APETALA1 (ZAPI) cDNA.

XX Floral meristem identity gene; APETALA1; API; ZAPI;

XX transgenic plant; angiosperm; seed development; maize; ds.

XX Zea mays.

XX Key Location/Qualifiers
 FH CDS 149..970
 FT /*tag= a

PN W09746078-A1.

PD 11-DEC-1997.

PF 05-JUN-1996; 96WO-US09453.

PR 05-JUN-1996; 96WO-US09453.

PA (REGC) UNIV CALIFORNIA.

PI Yanofsky MF;

DR MPI: 1998-041770/04.
 P-PSDB; AAW39134.

XX Nucleic acids encoding API floral meristem identity gene product
 PT from cauliflower and maize - useful for promoting early reproductive
 PT development and controlling the time of seed-derived crop harvest in
 PT e.g. grapes, beans, corn, wheat, etc

XX Claim 2; Page 125-127; 156pp; English.

XX This sequence comprises maize APETALA (ZAPI) cDNA, which encodes
 CC a floral meristem identity gene product (see AAW39134) that is
 CC involved in the conversion of shoot meristem to floral meristem.
 CC It was isolated from an immature ear cDNA library using
 CC Arabidopsis API cDNA (see AAV02760) as probe, and is suggested to be
 CC the maize orthologue of API. Mutation of the API gene results in
 CC replacement of basal flowers by inflorescence shoots that are not

CC subbanded by flowers. The invention relates to an expression
 CC vector comprising a nucleic acid sequence encoding a floral
 CC meristem gene product operably linked to a heterologous regulatory
 CC element (see AAV02770-75). The floral meristem gene product is
 CC selected from API, LFY (LEAFY) and CAL (CAULIFLOWER) (see AAV02760-67).
 CC The expression vector is used to convert shoot meristem tissue to
 CC floral meristem tissue in transgenic plants, especially angiosperms
 CC or gymnosperms, thereby promoting early reproductive development in
 CC these plants. This can be used to manipulate the time of crop
 CC harvest and to hasten breeding time.

CC Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

CC Query Match 50.7%; Score 300.4; DB 19; Length 1345;

CC Best Local Similarity 92.4%; Pred. No. 3.3e-75;

CC Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

CC 252 GAATCAGATATGGTCCGCGCAAGTGCAGTCAAGCGATAGAACAAATTAATC 311

CC 138 GCAACAGCGCATGGGCGCCGCAAGTACAGTGAAGCGATAGAACAAATTAATC 197

CC 312 GCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAGCGCGCATCTCCG 371

CC 198 GCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAGCGCGCATCTCCG 257

CC 372 TCCCTGTGACCGCGAGTCCGCGTATGCTCTTCCCGCAAGGCGCATCTTATGAGT 431

CC 258 TCCCTGTGACCGCGAGTCCGCGTATGCTCTTCCCGCAAGGCGCATCTTATGAGT 317

CC 432 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTTATGCTG 491

CC 318 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTTATGCTG 377

CC 492 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGCTCCAGATACAGA 551

CC 378 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGCTCCAGATACAGA 437

CC 552 AACTTAAGCGGAAGATTGAGACCATACAAATTAATGTCACAGC 593

CC 438 AACTGAAGGCCAAATTAAGACCATACAAATTAATGTCACAGC 479

RESULT 7

AAV06021 standard; cDNA; 1345 BP.

AAV06021;

08-JUN-1998 (first entry)

Maize floral meristem identity gene APTALAI orthologue cDNA.

Floral meristem identity gene; APTALAI; API; ZAP1; maize;

transgenic plant; angiosperm; seed development; ds.

Zea mays.

Key Location/Qualifiers

CDS 149..970

/*tag= a

11-DEC-1997.

04-JUN-1997; 97MO-US09682.

05-JUN-1996; 96US-0659188.

(REGC) UNIV CALIFORNIA.

Yanofsky MF;

DR WPI; 1998-041771/04.
 DR P-PDB; AAW43329.
 XX Use of floral meristem identity genes to convert shoot meristem to
 PT floral meristem - for promoting early reproductive development in
 PT the plants and control timing of seed-derived crop harvest (s) in
 PT e.g. grapes, beans, corn and wheat
 XX Claim 6; Page 110-112; 147pp; English.

XX This sequence comprises maize ZAP1 cDNA, which encodes a floral

CC meristem identity gene product (see AAW43329) that is involved in the

CC conversion of shoot meristem to floral meristem. It was isolated

CC from an immature ear cDNA library using Arabidopsis API cDNA (see

CC AAV06018) as probe, and is suggested to be the maize orthologue of API.

CC Mutation of the API gene results in replacement of basal flowers by

CC inflorescence shoots that are not subtended by flowers. The

CC invention relates to a recombinant nucleic acid molecule that

CC comprises an inducible regulatory element (see AAV06025-28) operably

CC linked to a nucleic acid molecule (see AAV06018-24) encoding a floral

CC meristem identity gene product (see AAW43326-32), especially API,

CC CAULIFLOWER (CAL) or LEAFY (LFY). The nucleic acids are used to

CC convert shoot meristem tissue into floral meristem tissue in

CC transgenic plants, thereby promoting early reproductive development

CC in these plants. This can be useful for manipulating the time of

CC crop harvest in seed-derived crops and to hasten breeding time.

CC Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

CC Query Match 50.7%; Score 300.4; DB 19; Length 1345;

CC Best Local Similarity 92.4%; Pred. No. 3.3e-75;

CC Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

CC 252 GAATCAGATATGGTCCGCGCAAGTGCAGTCAAGCGATAGAACAAATTAATC 311

CC 138 GCAACAGCGCATGGGCGCCGCAAGTACAGTGAAGCGATAGAACAAATTAATC 197

CC 312 GCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAGCGCGCATCTCCG 371

CC 198 GCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAGCGCGCATCTCCG 257

CC 372 TCCCTGTGACCGCGAGTCCGCGTATGCTCTTCCCGCAAGGCGCATCTTATGAGT 431

CC 258 TCCCTGTGACCGCGAGTCCGCGTATGCTCTTCCCGCAAGGCGCATCTTATGAGT 317

CC 432 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTTATGCTG 491

CC 318 ACGCCACCGACTCCAGCATGACAAATTTCTGAACGTTATGAGCGCTATCTTATGCTG 377

CC 492 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGCTCCAGATACAGA 551

CC 378 AAAAGGCTTTATTTAGCTGAATCTGAAGTGAAGGAAATTTGCTCCAGATACAGA 437

CC 552 AACTTAAGCGGAAGATTGAGACCATACAAATTAATGTCACAGC 593

CC 438 AACTGAAGGCCAAATTAAGACCATACAAATTAATGTCACAGC 479

RESULT 8

AAV061410 standard; cDNA; 1345 BP.

AAV061410;

19-FEB-2001 (first entry)

cDNA encoding a APTALAI (API) polypeptide.

APTALAI; API; floral meristem identity gene; CAULIFLOWER; CAL; LEAFY;

LFY; floral meristem; early flowering; ds.

Zea mays.

FH Key Location/Qualifiers
 FT CDS 149..970
 FT /*tag= a
 FT /product= "APETALAI"
 XX
 XX US6127123-A.
 XX
 XX 03-OCT-2000.
 XX
 XX 09-SEP-1998; 98US-0149976.
 XX
 XX 26-JAN-1996; 96US-0592214.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Yanofsky MF;
 XX
 XX MPI: 2000-618379/59.
 XX P-PSDB: AAB19244.
 XX
 XX Identifying a Brassica having a cauliflower phenotype involves
 XX detecting a polymorphism associated with cauliflower locus comprising a
 XX modified cauliflower allele that does not encode active cauliflower
 XX gene product -
 XX
 XX Example 1; Fig 4A-B; 93pp; English.
 XX
 XX The present sequence encodes an APETALAI (Api) polypeptide. The Api
 XX polypeptide is an ectopically expressible floral meristem identity
 XX gene product. The specification also describes CAULIFLOWER (CAL) and
 XX LEAFY (LFY) gene products. CAL is involved in the conversion of shoot
 XX meristem to floral meristem. CAL is highly conserved among different
 XX angiosperms. The CAL polynucleotides may be used to shoot meristem to
 XX floral meristem, and to promote early flowering in angiosperms.
 XX
 XX Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;
 XX
 XX Query Match 50.7%; Score 300.4; DB 21; Length 1345;
 XX Best Local Similarity 92.4%; Pred. No. 3.3e-75;
 XX Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 XX
 XX 252 GAAATCAGATATGGGTGCGCGCAAGGTGACGTGAGCGGATAGAACAAAGATTAATC 311
 XX |||||
 XX 138 GCAACAGGCGATGGGCGCGCAAGGTACAGCTAAGCGGATAGAACAAAGATTAACC 197
 XX |||||
 XX 312 GGCAGGTACCTTCTCCAAAGCGCGCAAGGGCTCTGTAAGAGCGGACGATCTCCG 371
 XX |||||
 XX 198 GGCAGGTACCTTCTCCAAAGCGCGCAAGGGCTCTGTAAGAGCGGACGATCTCCG 257
 XX |||||
 XX 372 TCCTCTGTAAGCGGAGGTGCGCGTCAATGCTCTTCTCCCAAGGCAAGCTTATGAGT 431
 XX |||||
 XX 258 TCCTCTGTAAGCGGAGGTGCGCGTCAATGCTCTTCTCCCAAGGCAAGCTTATGAGT 317
 XX |||||
 XX 432 ACGCCACCGACTCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 491
 XX |||||
 XX 318 ACGCCACCGACTCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 377
 XX |||||
 XX 492 AAAAGGCTCTTATTTCACTGATGTAATCTGAAGTGAAGGAAATTTGGTCCCAAGTACAGA 551
 XX |||||
 XX 378 AAAAGGCTCTTATTTCACTGATGTAATCTGAAGTGAAGGAAATTTGGTCCCAAGTACAGA 437
 XX |||||
 XX 552 AACTTAAGCGCAAGATTGAGACCATACAAAATTTGTCACAAGC 593
 XX |||||
 XX 438 AACTGAAGCGCAAAATTTGAGACCATACAAAATTTGTCACAAGC 479
 XX |||||
 XX
 XX RESULT 9
 XX ID AA257057 standard; DNA; 1345 BP.
 XX AC AA257057;
 XX DT 19-MAY-2000 (first entry)

XX Zea mays ZAPI protein encoding DNA.
 XX DE
 XX Seed plant; floral meristem; mutation; TPL gene; CAL;
 XX reproduction; plant breeding; Api protein; ds.
 XX
 XX Zea mays.
 XX
 XX US6025543-A.
 XX
 XX 15-FEB-2000.
 XX
 XX 05-JUN-1996; 96US-0655241.
 XX
 XX 05-JUN-1996; 96US-0655241.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX
 XX Yanofsky MF;
 XX
 XX MPI: 2000-181843/16.
 XX P-PSDB: AAV67553.
 XX
 XX New transgenic seed plant exhibiting early reproductive development
 XX comprises a CAULIFLOWER encoding nucleic acid and a non-mutant
 XX endogenous TERMINAL FLOWER gene -
 XX
 XX Example 5; Columns 59-64; 51pp; English.
 XX
 XX The invention relates to a new non-naturally occurring seed plant that
 XX comprises a first ectopically expressible nucleic acid molecule encoding
 XX a floral meristem identity gene product, provided that the seed plant
 XX does not contain a mutation in an endogenous TERMINAL FLOWER (TFL) gene
 XX that results in ectopic expression of CAL. The non-naturally occurring
 XX seed plant exhibits early reproductive development. The method of
 XX promoting early reproductive development can make breeding of long
 XX generation seed plants such as trees practical. The method can be used to
 XX increase floral meristem identity gene product expression in different
 XX crop fields at different times, resulting in a staggered time of harvest
 XX for the different fields. The present sequence represents a Zea mays
 XX Api protein encoding DNA.
 XX
 XX Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;
 XX
 XX Query Match 50.7%; Score 300.4; DB 21; Length 1345;
 XX Best Local Similarity 92.4%; Pred. No. 3.3e-75;
 XX Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
 XX
 XX 252 GAAATCAGATATGGGTGCGCGCAAGGTGACGTGAGCGGATAGAACAAAGATTAATC 311
 XX |||||
 XX 138 GCAACAGGCGATGGGCGCGCAAGGTACAGCTAAGCGGATAGAACAAAGATTAACC 197
 XX |||||
 XX 312 GGCAGGTACCTTCTCCAAAGCGCGCAAGGGCTCTGTAAGAGCGGACGATCTCCG 371
 XX |||||
 XX 198 GGCAGGTACCTTCTCCAAAGCGCGCAAGGGCTCTGTAAGAGCGGACGATCTCCG 257
 XX |||||
 XX 372 TCCTCTGTAAGCGGAGGTGCGCGTCAATGCTCTTCTCCCAAGGCAAGCTTATGAGT 431
 XX |||||
 XX 258 TCCTCTGTAAGCGGAGGTGCGCGTCAATGCTCTTCTCCCAAGGCAAGCTTATGAGT 317
 XX |||||
 XX 432 ACGCCACCGACTCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 491
 XX |||||
 XX 318 ACGCCACCGACTCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTTATGCTG 377
 XX |||||
 XX 492 AAAAGGCTCTTATTTCACTGATGTAATCTGAAGTGAAGGAAATTTGGTCCCAAGTACAGA 551
 XX |||||
 XX 378 AAAAGGCTCTTATTTCACTGATGTAATCTGAAGTGAAGGAAATTTGGTCCCAAGTACAGA 437
 XX |||||
 XX 552 AACTTAAGCGCAAGATTGAGACCATACAAAATTTGTCACAAGC 593
 XX |||||
 XX 438 AACTGAAGCGCAAAATTTGAGACCATACAAAATTTGTCACAAGC 479
 XX |||||

RESULT 10
22703144

AAZ92144
ID AAZ92144 standard; cDNA; 1345 BP.

AC AAZ92144;

DT 19-MAY-2000 (first entry)

Corn APETALA1 (API) nucleotide sequence.

KM APEPALAI; API, floral meristem identity; early reproductive development;
KM transgenic plant; selective breeding programme; disease resistance;
KM corn; ds.

Zea mays.

PN US6025483-A.

PD 15-FEB-2000.

05-JUN-1996; 96US-0655227.

PR 05-JUN-1996; 96US-0655227.

PA (REGC) UNIV CALIFORNIA.

PI Yanofsky MF;

WPI; 2000-181839/16.

33 X

PT reproductive development in seed plants, useful for accelerating

XX
XX

CC This sequence represents the APETALA1 (AP1) gene sequence from corn. AP1
CC is a floral meristem identity product, that promotes conversion of shoot
CC meristem to floral meristem in an angiosperm. Vectors containing the AP1
CC gene can be used to create transgenic plants. AP1 nucleotide sequences
CC can be used to promote early reproductive development in seed plants
CC which is useful for accelerating selective breeding programmes that
CC require several rounds of crossing to produce plants with disease and
CC insect resistance. The nucleotide sequences are particularly useful for
CC promoting early reproductive development in long generation seed plants
CC such as trees.

Sequence 1345 BP; 349 A; 373 C; 358 G; 265 T; 0 other;

Query Match 50.7%; Score 300.4; DB 21; Length 1345;

Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

OY	252	GAATATCAGATATATGGCTCCCGCAGAGGTGACGTGAACGCATATAGAAACAATTAATC	311
Db	138	GCACAAGGCAGATGGGGCCCGCAGAGTACAGCTGAAGCCGATATAGAAACAATTAACC	197
OY	312	GGCAGGTGACTTCTTCCAAAGCCGCGCACAAGGCTCTCTGAAGAAGCGCAAGATCTCCG	371
Db	198	GGCAGGTGACTTCTTCCAAAGCCGCGCGCAAGCCCTGCTCAAGAGGCGCACAGATCTCCG	257
OY	372	TCCTCGTACGCGAGGTGCGCCGTATCGTCTTCTCCCCCAAGCGAACCTGTATAGT	431
Db	258	TCCTCTGCGATGCGAGGTGCGCCGTATCGTCTTCTCCCCCAAGCGAACCTGTACGAGT	317
OY	432	ACGCCACCGACTCCAGCATGACAAAATCTTGAACGTATAGACCGCTACTCTTATGCTG	491
Db	318	ACGCCACCGACTCCCCCATAGAACAAATCTTGAACGCTATGACGATATCTCTATGCTG	377
OY	492	AAAAGCTCTTATTTACGCTGAATCTGAAGTAGAGGAATATGCTGCACGAATACAGGA	551
Db	378	AAAAGCTCTTATTTACGCTGAATCTGAAGTAGAGGAATATGCTGCACGAATACAGGA	437

Qy 552 AACTTAAGCGCAAGATTGAGACCATACAAAAATGTCAAGC 593
Db 438 AACTGAAGGCCAAATTGAGACCATACAAAAATGCCAAGC 479

RESULT 11
PAGE 740

ID	AAF75749	standard; DNA; 1289 BP.
xx		

AC AAF75749
VY

DT 14-MAY-2001 (first entry)
VY

Rice MADS box gene.

KW Rice; MADS box; plant branching regulation; agriculture; ds.

OS *Oryza sativa*.

PN WO200114559-A1

PD 01-MAR-2001.

PF 18-AUG-2000; 2000WO-JP05537

PR 19-AUG-1999; 99JP-0232318

PA (TSUB) KUMIAI CHEM IND CO LTD.
DA (KOTI /) KOTIMA M

XX
XX

XX
WB1: 3001-191647/19
DB

DR P-PSDB; AAB73250.
XY

PT Rice MADS box gene 1

PT Rice MADS box gene for regulating plant branching to provide ornamental
PT or agricultural plants with value-added properties or increase in yield
PT -
PS Claim 3; Page 19-20; 43pp; Japanese.
XX

PS Claim 3; Page 19-20; 43pp; Japanese.

CC The present sequence is a gene which contains the rice MADS box gene.
CC This sequence can be used for regulating plant branching to provide
CC ornamental or agricultural plants. In addition, plants with value-added
CC properties or an increased yield can be produced using the present
CC sequence.

SQ Sequence 1289 BP; 354 A; 316 C; 337 G; 282 T; 0 other;

Query Match	47.88;	Score 283.2;	DB 22;	Length 1289,
-------------	--------	--------------	--------	--------------

Matches 306; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

OY	250	GCGAAATCAGATATGGGTTCGCGCAGAGTCAGCTGAAACCGGATAGAGAAACAAGATAA	309
Db	112	GGAGCGCGGAGATGGGCGCGGGGAAAGTGCAGCTGAAGCGGATAGAGAACAAAGATCAA	171
OY	310	TCGGCAGGTACCTTTCTCCAGCGCCGCAACGGGCTCCTGAAAGAGCGCCACAGATATTC	369
Db	172	CAGGACAGGTGACGTTCTCCAAAGAGGAAATGGATTTGCTGAAGAAAGGCCACGAGATCTC	231
OY	370	CGTCCTCTGTACGGGAGGATCGCCGATCGTCTTCTCCCCAAAGCGAACCTCATATGA	429
Db	232	CGTCTCTGCGACCGCCGAGTGTCGCCCATCGTCTTCTCCCAAGGCGAACCTCATACGA	291
OY	430	GTAAGCCACCGACTCCAGCATGAGCAAAATTTTGAACGTTATGAGCGCTACTTTATGC	489
Db	292	GTAAGCCACTGACTCCAGATGAGCAAAATCCTTGAAGTTATGAGCGCTACTTTCAATATGC	351
OY	490	TGAAAGGCTCTTATTTGAGCTGAAATCGAAAGTAGGGAATTTGGTCCAGATATACAG	549
Db	352	TGAAAGGCTCTTATTTGAGCTGAAATCCGAGATAGGGAATTTGGTCCATGAAATACAG	411

OY 550 GAACTTAAGCGAAGATTGAGACCATACAAAATGTCACAAAC 593
 DB 412 GAACTTAAGCGAAGATTGAGACCATACAAAATGTCACAAAC 455

RESULT 12

AAC41059
 AAC41059 standard; DNA; 466 BP.

AC AAC41059;

DT 17-OCT-2000 (first entry)

DE Zea mays DNA fragment SEQ ID NO: 30499.

XX Hybridisation assay; genetic mapping; gene expression control;
 KM protein identification; signal transduction pathway; metabolic;
 KM pathway; promoter; termination sequence; corn; ss.

XX Zea mays subsp. mays.

XX EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0125548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

XX PR 01-APR-1999; 99US-0127462.

XX PR 06-APR-1999; 99US-0128234.

XX PR 08-APR-1999; 99US-0128714.

XX PR 16-APR-1999; 99US-0129845.

XX PR 19-APR-1999; 99US-0130077.

XX PR 21-APR-1999; 99US-0130449.

XX PR 23-APR-1999; 99US-0130510.

XX PR 23-APR-1999; 99US-0130891.

XX PR 28-APR-1999; 99US-0131449.

XX PR 30-APR-1999; 99US-0132048.

XX PR 30-APR-1999; 99US-0132407.

XX PR 04-MAY-1999; 99US-0132484.

XX PR 05-MAY-1999; 99US-0132485.

XX PR 06-MAY-1999; 99US-0132486.

XX PR 07-MAY-1999; 99US-0132487.

XX PR 11-MAY-1999; 99US-0132863.

XX PR 14-MAY-1999; 99US-0134256.

XX PR 14-MAY-1999; 99US-0134218.

XX PR 14-MAY-1999; 99US-0134219.

XX PR 14-MAY-1999; 99US-0134221.

XX PR 14-MAY-1999; 99US-0134370.

XX PR 18-MAY-1999; 99US-0134768.

XX PR 19-MAY-1999; 99US-0134941.

XX PR 20-MAY-1999; 99US-0135124.

XX PR 21-MAY-1999; 99US-0135353.

XX PR 24-MAY-1999; 99US-0135629.

XX PR 25-MAY-1999; 99US-0136021.

XX PR 27-MAY-1999; 99US-0136392.

XX PR 28-MAY-1999; 99US-0136782.

XX PR 01-JUN-1999; 99US-0137222.

XX PR 03-JUN-1999; 99US-0137528.

XX PR 04-JUN-1999; 99US-0137502.

XX PR 07-JUN-1999; 99US-0137724.

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RESULT 13

AA134430 standard; cDNA; 1032 BP.

AA134430;

01-OCT-1996 (first entry)

Eucalyptus SOE2S cDNA.

Eucalyptus; reproductive gene; SOE2S; Arabidopsis; agamous gene;

Antirrhinum; plena gene; sterility; fertility; forest tree;

transgenic plant; flower development; antisense; ribozyme; ss.

Eucalyptus globulus.

Key Location/Qualifiers

FT 184..801

FT CDS /tag= a

FT /product= SOE-2S

PN AU9539013-A.

PD 30-MAY-1996.

PF 22-NOV-1995; 95AU-0039013.

PR 22-NOV-1994; 94AU-0009589.

PA (GSTR) COMMONWEALTH SCI & IND RES ORG.

PI Dennis ES, Harcourt RL, Kyoizuka J, Llewellyn D;

PI Peacock WJ, Southerton S;

DR WPI; 1996-278411/29.

DR P-PSDB; AAR9635.

PT Eucalyptus reproductive genes - useful for prodn. of sterile

PT Eucalyptus trees useful for establishing wood lot plantations or in

PT re-forestation projects

PS Claim 8; Page 34-35; 60pp; English.

CC cDNA clones SOE1 (AA134429), SOE2S (AA134430) and SOE2L (AA134431) were

CC identified by homology to the MADS box of the Arabidopsis apical

CC 1 (AP1) and Antirrhinum squamosa (SQUA) flower development genes.

CC They were obd. by PCR amplification of E. globulus DNA using

CC primers based on the MADS box of the Arabidopsis and Antirrhinum

CC genes, followed by screening of a E. globulus young flower bud

CC library. The SOE2S cDNA codes for protein SOE2-S (AAR9635).

CC Antisense or ribozyme constructs of SOE, or of FLE2 and SOE genes

CC (see also AA134426, AA134428 and AA134432), may be used to produce

CC sterile transgenic Eucalyptus trees by minimising inflorescence.

XX Sequence 1032 BP; 299 A; 231 C; 263 G; 239 T; 0 other;

Query Match 32.9%; Score 195; DB 17; Length 1032;
 Best Local Similarity 71.8%; Pred. No. 2.6e-45;

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Search completed: June 29, 2003, 07:29:46
 Job time : 162 secs

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RESULT 2

US-08-659-188-7

Sequence 7, Application US/08659188

Patent No. 6002069

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/659,188

FILING DATE: 05-JUN-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 1946

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1345 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 149..968

NAME/KEY: misc feature

LOCATION: 1..1345

OTHER INFORMATION: /note="product = Zea mays AP1."

US-08-659-188-7

Query Match

Best Local Similarity 92.4%; Score 300.4; DB 3; Length 1345;

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RESULT 3

US-08-655-227-7

Sequence 7, Application US/08655227

Patent No. 6025483

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Maize and Cauliflower APTAL1 Gene

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/655,227

FILING DATE: 05-JUN-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2143

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-8949

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1345 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 149..968

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Sequence 13, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditlea, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 756
TYPE: DNA
ORGANISM: Brassica oleracea var. botrytis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(453)
OTHER INFORMATION: CAULIFLOWER
US-09-853-450-13

Query Match 22.2%; Score 131.4; DB 9; Length 756;
Best Local Similarity 66.0%; Pred. No. 8e-32;
Matches 208; Conservative 0; Mismatches 101; Indels 6; Gaps 1;

QY 263 ATGGGTGCGGCAAGTGTGACGCTGAAAGGAGTATGAGCAAGATTAATCGCAGGTGAC 322
DB 1 ATGGGAAGAGGAGTATGAGTGAATGAAAGAGATGAGCAAGATTAATCGCAGGTGAC 60
QY 323 TTCTCCAAAGCGCCGCAACGGCTCTCTGAAGAGGCGCAGATCTCCGTCTCTGTAC 382
DB 61 TTTCGAAAAGGCTGAGGCTTTGTAAGAAAGCCATGAGATCTCAATCTTTGTAT 120
QY 383 GCGAGGTGCGGCTGATGCTCTTCTCCCAAGGCAAGCTCTATGATGAGCCACCGAC 442
DB 121 GCTGAAGTTCCTCTATGCTCTTCTCCATAGGGGAACTGTGAGTACTCGCTGAA 180
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGGCTCT 502
DB 181 TCTTGATGAGAGAGTACTGAAAGCTACGAGAGTACTCTTACGCGAAGAAAGCTA 240
QY 503 ATTTCAGTGAATCTGAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 556
DB 241 AAAGCTCCAGCTCTCAGCTCAATGCAAGAAAGAACTGCTCAATGCAATATAGAGGCTT 300
QY 557 AAGGCAAGATTGAG 571
DB 301 AAGGCTAAGATTGAG 315

RESULT 13
US-09-853-450-27
Sequence 27, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditlea, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 747
TYPE: DNA
ORGANISM: Arabidopsis thaliana

FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(747)
OTHER INFORMATION: SEPALLATA1 (SEP1)
US-09-853-450-27

Query Match 19.4%; Score 114.8; DB 9; Length 747;
Best Local Similarity 60.1%; Pred. No. 1.7e-26;
Matches 191; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 263 ATGGGTGCGGCAAGTGTGACGCTGAAAGGAGTATGAGCAAGATTAATCGCAGGTGAC 322
DB 1 ATGGGAAGAGGAGTATGAGTGAATGAAAGAGATGAGCAAGATTAATCGCAGGTGAC 60
QY 323 TTCTCCAAAGCGCCGCAACGGCTCTCTGAAGAGGCGCAGATCTCCGTCTCTGTAC 382
DB 61 TTTCGAAAAGGCTGAGGCTTTGTAAGAAAGCCATGAGATCTCAATCTTTGTAT 120
QY 383 GCGAGGTGCGGCTGATGCTCTTCTCCCAAGGCAAGCTCTATGATGAGCCACCGAC 442
DB 121 GCTGAAGTTCCTCTATGCTCTTCTCCATAGGGGAACTGTGAGTACTCGCTGAA 180
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAAAGGCTCT 502
DB 181 TCAAGATGCTCAAGACACTTATGCTGATGAGCAAGATTAATGATGATGATGAGTAC 240
QY 503 ATTTCAGTGAATCTGAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 562
DB 241 AACAAACCTGCGCAAGAACTTGAGACAGCTACAGAAATATCTGAAGCTTAAGGT 300
QY 563 AAGATTGAGACATACAA 580
DB 301 AGATTGAGAACTTCAA 318

RESULT 14
US-09-853-450-29
Sequence 29, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditlea, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 29
LENGTH: 753
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(753)
OTHER INFORMATION: SEPALLATA2 (SEP2)
US-09-853-450-29

Query Match 18.5%; Score 110; DB 9; Length 753;
Best Local Similarity 59.1%; Pred. No. 5.7e-25;
Matches 188; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 263 ATGGGTGCGGCAAGTGTGACGCTGAAAGGAGTATGAGCAAGATTAATCGCAGGTGAC 322
DB 1 ATGGGAAGAGGAGTATGAGTGAATGAAAGAGATGAGCAAGATTAATCGCAGGTGAC 60
QY 323 TTCTCCAAAGCGCCGCAACGGCTCTCTGAAGAGGCGCAGATCTCCGTCTCTGTAC 382
DB 61 TTTCGAAAAGGCTGAGGCTTTGTAAGAAAGCCATGAGATCTCAATCTTTGTAT 120

US-09-853-450-5

Query Match 26.4%; Score 156.6; DB 9; Length 768;
 Best Local Similarity 67.1%; Pred. No. 6.8e-40;
 Matches 222; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

253 ATGGTCCGCGCAAGTGTGACGCTGAACCGGATAGAACAAATATGCGAGGTGACC 322
 1 ATGGGAAGGGGTAGGGTTCAGTTGAAGAGATAGAAACAAATCAATGACAACTGACAC 60
 323 TTCTCCAAAGCCGCGCAAGGGGCTCCGGAAGAGGGGCAAGATCTCCGCTCTGTGAC 382
 61 TTCTGAAAAGAGAGCTGTCTTATGAAGAAAGCTCATGAGATCTCTGTCTGTGAT 120
 383 GCGGAGGTGCGCGTATCTCTTCTCCCAAGGCAAGCTCTATGATGACCCACCGAC 442
 121 GCTGAAGTTGGCGCTTGTGTCTTCTCCCAAGGGGAACTTTGAATACCCCACTGAT 180
 443 TCCAGCATGACAAATTTTGAAGCTTATGAGCCGCTCTTATGCTGAAGAGCTCTT 502
 181 TCTTATGAGAGAGATCTTGAAGCTATGAGAGATCTTACGCGCAGAGACAGCTT 240
 503 ATTGAGCTGATCTGAAGAGTGAAGGAAATTTGTCGCAAGATACAGAACTTAAGCG 562
 241 ATGCACTGAGTCCGACTCCAAATGCAACTGTGATGAGATATATGAGCTTAAGCT 300
 563 AAGATTGAGACCATCAAAATATGTCACAGC 593
 301 AAGATTGAGCTTTTGAAGAGAAACCAAGGC 331

RESULT 10

US-09-853-450-9
 ; Sequence 9, Application US/09853450
 ; Publication No. US20020194645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Pelaz, Soraya
 ; APPLICANT: Ditlea, Gary
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
 ; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
 ; FILE REFERENCE: 19452A-002400US
 ; CURRENT APPLICATION NUMBER: US/09/853,450
 ; CURRENT FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 779

TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (10)..(777)
 OTHER INFORMATION: CAULIFLOWER (CAL)
 NAME/KEY: modified base
 LOCATION: (778)..(779)
 OTHER INFORMATION: n = g, a, c or t

Query Match 24.5%; Score 145.2; DB 9; Length 779;
 Best Local Similarity 66.5%; Pred. No. 3.1e-36;
 Matches 226; Conservative 0; Mismatches 108; Indels 6; Gaps 1;

260 GATATGGTCCGCGCAAGTGTGACGCTGAACCGGATAGAACAAATATGCGAGGTG 319
 7 GAAATGGGAAGGGGTAGGGTTCAGTTGAAGAGATAGAAACAAATCAATGACAACTG 66
 320 ACCTTCCAAAGCCGCGCAAGGGGCTCCGGAAGAGGGGCAAGATCTCCGCTCTGT 379
 67 ACATTTCTGAAAAGAGAGCTGTCTTTGAAGAAAGCTCAGAGATCTCTGTCTTTGT 126
 380 GACGCGAGGTGCGCGTATCTTCTCCCAAGGCAAGCTCTATGATGACCGCAC 439

127 GATGCGGAGGTTCCCTTATGTCTTCTCCCATAGGGCAATTTGTGAGATCTCT 186

440 GACTCCAGCATGAGCAAAATCTTGAAGCTTATGAGCGCTACTTATGCTGAAGAGCT 499

187 GATTTTCATGAGAGAGAGTACTGAGACGCTACGAGAGTATTTCTTACCGCAGAGAC 246

500 CTATATTCAGTGAATCTGAAGAGGGA-----AATGTGTCACGAATACAGAA 553

247 CTGATGACCTGACTCTCAGTTATGCAACAGAGAACTGTCAATGAGATATGACAG 306

554 CTTAAGCGGAAGTTGAGACCATACAAATATGTCACAGC 593

307 CTTAAGCGCAAGATTGAGCTTTTGAAGAGAAACCAAGGC 346

RESULT 11

US-09-853-450-11
 ; Sequence 11, Application US/09853450
 ; Publication No. US20020194645A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yanofsky, Martin F.
 ; APPLICANT: Pelaz, Soraya
 ; APPLICANT: Ditlea, Gary
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
 ; TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
 ; FILE REFERENCE: 19452A-002400US
 ; CURRENT APPLICATION NUMBER: US/09/853,450
 ; CURRENT FILING DATE: 2001-05-09
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 756
 ; TYPE: DNA
 ORGANISM: Brassica oleracea
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(756)
 OTHER INFORMATION: CAULIFLOWER

Query Match 22.4%; Score 132.6; DB 9; Length 756;
 Best Local Similarity 64.4%; Pred. No. 3.3e-32;
 Matches 217; Conservative 0; Mismatches 114; Indels 6; Gaps 1;

263 ATGGTCCGCGCAAGTGTGACGCTGAACCGGATAGAACAAATATGCGAGGTGACC 322

1 ATGGGAAGGGGTAGGGTTCAGTTGAAGAGATAGAAACAAATCAACCGCAAGTGC 60

323 TTCTCCAAAGCCGCGCAAGGGGCTCCGGAAGAGGGGCAAGATCTCCGCTCTGTGAC 382

61 TTCTGAAAAGAGAGCTGTCTTATGAAGAAAGCTCATGAGATCTCTGTGTGAT 120

383 GCGGAGGTGCGCGTATCTCTTCTCCCAAGGCAAGCTCTATGATGACCCACCGAC 442

121 GCTGAGGTTTCCCTTATGTCTTCTCCCATAGGGGAACTGTGAGTACTCTGTGAA 180

443 TCCAGCATGACAAATTTTGAAGCTTATGAGCGCTACTTATGCTGAAGAGCTCTT 502

181 TCTTCAATGAGAGAGTACTGAAACACTACGAGAGTACTTTCAGCGCGAGAAACAGCTA 240

503 ATTGAGTGAATCTGAAGAGGGA-----AATGTGTCACGAATACAGAAACTT 556

241 AAGCTTCAGACTCTCAGTCAATGCAACAAAGAACTGTGATGAGATATATGACAGCTT 300

557 AAGCGAAGATTGAGACCATACAAATATGTCACAGC 593

301 AAGCTTAAGATTGAGCTTTTGAAGAGAAACCAAGGC 337

RESULT 12

US-09-853-450-13

OY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 7

US-09-978-740A-1

; Sequence 1, Application US/09978740A
; Publication No. US2003005481A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Niggin Biosynthesis in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000960US
; CURRENT APPLICATION NUMBER: US/09/978,740A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-740A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

OY 260 GATATGGTCCGCGCAAGTGCAGTGAAGCGGATGAGCAAGATTAATCGCAGGTG 319
DB 98 GATATGGAGAGAGTGAAGGTTCACTGAGAGAGATGAGAAACAGATCAATGAGCAAGTT 157
OY 320 ACCTTCTCCAGCGCGCGCAAGGCGCTCTGAAAGAGGCGACGAGATCTCCGTCCTGT 379
DB 158 ACTTCTCAAGAGAGAGTCTGCTTCTGCTCAAGAGCTCAAGATCTCTGTCG 217
OY 380 GACGCGAGGTGCGCGTATGCTCTTCTCCCAAGGCAAGCTCTATGAGTACGCCACC 439
DB 218 GATGCTGAGTGTGCTCTATGCTCTTCTTCCAAAGCAACTTGAATATTCACAC 277
OY 440 GACTTCAGATGAGCAAAATTTGAAAGCTTATGAGCGGCTACTTATGCTGAAGAGCT 499
DB 278 GACTTCTGATGAGAGAGTACTTGAAGCTATGCTATTTATTTATTCAGACAAACA 337
OY 500 CTATTTAGCTGATCTGAAGTGAAGGAAATTTGTCGACGATAGCAAGAACTTAAG 559
DB 338 CTGTTGGCCGAGAGCTTTCAAAAGTGAATGGGTTTGAACAATGCTAAGCTCAAG 397
OY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 8

US-09-978-730-1

; Sequence 1, Application US/09978730
; Patent No. US20020129403A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegren, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Niggin Biosynthesis in Transgenic

; TITLE OF INVENTION: Plants
; FILE REFERENCE: 19452A-000920US
; CURRENT APPLICATION NUMBER: US/09/978,730
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-730-1

Query Match 26.7%; Score 158.4; DB 10; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

OY 260 GATATGGTCCGCGCAAGTGCAGTGAAGCGGATGAGCAAGATTAATCGCAGGTG 319
DB 98 GATATGGAGAGAGTGAAGGTTCACTGAGAGAGATGAGAAACAGATCAATGAGCAAGTT 157
OY 320 ACCTTCTCCAGCGCGCGCAAGGCGCTCTGAAAGAGGCGACGAGATCTCCGTCCTGT 379
DB 158 ACTTCTCAAGAGAGAGTCTGCTTCTGCTCAAGAGCTCAAGATCTCTGTCG 217
OY 380 GACGCGAGGTGCGCGTATGCTCTTCTCCCAAGGCAAGCTCTATGAGTACGCCACC 439
DB 218 GATGCTGAGTGTGCTCTATGCTCTTCTTCCAAAGCAACTTGAATATTCACAC 277
OY 440 GACTTCAGATGAGCAAAATTTGAAAGCTTATGAGCGGCTACTTATGCTGAAGAGCT 499
DB 278 GACTTCTGATGAGAGAGTACTTGAAGCTATGCTATTTATTTATTCAGACAAACA 337
OY 500 CTATTTAGCTGATCTGAAGTGAAGGAAATTTGTCGACGATAGCAAGAACTTAAG 559
DB 338 CTGTTGGCCGAGAGCTTTCAAAAGTGAATGGGTTTGAACAATGCTAAGCTCAAG 397
OY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 9

US-09-853-450-5

; Sequence 5, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Brassica oleracea var. botrytis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
; OTHER INFORMATION: APETALA1 (AP1)

FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-729A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 260 GATATGGGTCGGGCAAGGTGAGCTGAAGCGGATAGAGAAAGTAATGCGGAGGTG 319
DB 98 GATATGGGAGAGGATGAGGTTCAGCTGAAGAGATAGAGAAAGTAATGCGGAGGT 157
QY 320 ACCCTTCGCAAGCGCGCAACGGGCTCTGAAGAAAGCGCAGATCTCCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGAGGTCTGTGTTGCTCAAGAAAGCTCATGATCTCTGTTCTGC 217
QY 380 GACGCGGAGGTGCGGTCATGCTCTTCTCCCAAGGCAAGCTCTTATGATGAGCCACC 439
DB 218 GATGCTGAGGTGCTCTCATGCTCTTCTTCCAAAGGCAAGCTCTCGAATATTCAC 277
QY 440 GACTCCAGATGAGCAAAATTTGTAAGCTTATGAGCGCTACTTATGCTGAAGGCT 499
DB 278 GACTCTTGATGAGAGGATCTTGAAGCTATGATGCTATTTATTCAGACAAACA 337
QY 500 CTATATTCAGCTGAATCTGAAGTGAAGGAAATGCTGCGCAAGATACAGAACTTAAG 559
DB 338 CTGTGTCGCGAGAGCTTTCAAGAGTGAATTTGGTTCTTGAACATGCTAAGCTCAAG 397
QY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 5

US-09-981-087A-1
; Sequence 1, Application US/09981087A
; Patent No. US20020178466A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: Farrandiz, Cristina
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000940US
; CURRENT APPLICATION NUMBER: US/09/981,087A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-981-087A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 260 GATATGGGTCGGGCAAGGTGAGCTGAAGCGGATAGAGAAAGTAATGCGGAGGTG 319
DB 98 GATATGGGAGAGGATGAGGTTCAGCTGAAGAGATAGAGAAAGTAATGCGGAGGT 157

QY 320 ACCCTTCGCAAGCGCGCAACGGGCTCTGAAGAGCGCAGATTCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGGATGAGGTTCAGCTGAAGAGCTCATGATCTCTGTTCTGCG 217
QY 380 GACGCGGAGGTGCGGTCATGCTCTTCCCAAGGCAAGCTTATGATGAGCCACC 439
DB 218 GATGCTGAGGTGCTCTCATGCTCTTCTTCCAAAGGCAAGCTTGAATATTCACC 277
QY 440 GACTCCAGATGAGCAAAATTTGTAAGCTTATGAGCGCTACTTATGCTGAAGGCT 499
DB 278 GACTCTTGATGAGAGGATCTTGAAGCTATGATGCTATTTATTCAGACAAACA 337
QY 500 CTATATTCAGCTGAATCTGAAGTGAAGGAAATGCTGCGCAAGATACAGAACTTAAG 559
DB 338 CTGTGTCGCGAGAGCTTTCAAGAGTGAATTTGGTTCTTGAACATGCTAAGCTCAAG 397
QY 560 GCGAAGATTGAG 571
DB 398 GCAAGAGTTGAG 409

RESULT 6

US-09-978-382A-1
; Sequence 1, Application US/09978382A
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000930US
; CURRENT APPLICATION NUMBER: US/09/978,382A
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-382A-1

Query Match 26.7%; Score 158.4; DB 9; Length 1062;
Best Local Similarity 69.2%; Pred. No. 2.1e-40;
Matches 216; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 260 GATATGGGTCGGGCAAGGTGAGCTGAAGCGGATAGAGAAAGTAATGCGGAGGTG 319
DB 98 GATATGGGAGAGGATGAGGTTCAGCTGAAGAGATAGAGAAAGTAATGCGGAGGT 157
QY 320 ACCCTTCGCAAGCGCGCAACGGGCTCTGAAGAGCGCAGATCTCCGCTCTGT 379
DB 158 ACTTCTCAAGAGAGAGGTCTGTGTTGCTCAAGAAAGCTCATGATCTCTGTTCTGC 217
QY 380 GACGCGGAGGTGCGGTCATGCTCTTCTCCCAAGGCAAGCTCTTATGATGAGCCACC 439
DB 218 GATGCTGAGGTGCTCTCATGCTCTTCTTCCAAAGGCAAGCTTGAATATTCACC 277
QY 440 GACTCCAGATGAGCAAAATTTGTAAGCTTATGAGCGCTACTTATGCTGAAGGCT 499
DB 278 GACTCTTGATGAGAGGATCTTGAAGCTATGATGCTATTTATTCAGACAAACA 337
QY 500 CTATATTCAGCTGAATCTGAAGTGAAGGAAATGCTGCGCAAGATACAGAAACTTAAG 559
DB 338 CTGTGTCGCGAGAGCTTTCAAGAGTGAATTTGGTTCTTGAACATGCTAAGCTCAAG 397

Oy	432	AGCGCACCCGACCTCCACATGAGCAAAATCTTGAAGCTTATGAGGGCTACTTATGCTG	491
Db	318	AGCGCACCCGACCTCCCGCATGCAAAATCTTGAAGCTATGAGGATATTCCTATCTG	377
Oy	492	AAAAGGCTCTTATTTGAGCTGATCTGAAAGTGAGAGGAAATTTGGTGCACGAAATACAGA	551
Db	378	AAAAGGCTCTTATTTGAGCTGATCTGAAAGTGAGAGGAAATTTGGTGCACGAAATACAGA	437
Oy	552	AACTTAAGCGAGATTGAGACCATTCAAAAAATGTCAACAG	593
Db	438	AACTGAAGCGCAAAATTTGAGACCATCAAAAAATGCAACAG	479

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US-09-853-450-1
; Sequence 1, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE OF INVENTION: Exhibiting Modulated Reproductive Development
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ-ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1057
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(894)
; OTHER INFORMATION: APETALAL1 (AP1)
US-09-853-450-1

Query March 27.6%; Score 163.4; DB 9; Length 1057;
Best Local Similarity 68.2%; Pred. No. 5.3e-42;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0

Db
261 ATATGGCTCGCGCGCAAGGTGCAAGCCGATAGACAACAGATTAATCGGACGTGA 320
122 AAATGGGAAGGGGTAGGGTTCAATTGAAGAGATAGAGAACAAAGTCAATACAAAGTGA 181
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182 CATTTCCAAAAGGAAGAGCGTGGTCTTTTGAAAGAAAGCTCATGAGATCTCTGTTCTGTG 241
381 ACGCGGAGGTGCGCGCTCATCGTCTCTCTCCCAAGGCAAGCTCATGATGATGCGCACCG 440
242 ATGCTGAAGTGTCTCTGTGTCTCTCTCCATTAAGGGGAAACCTTCGAAATCTCCACTG 301
441 ACTCCAGCATGGAACAATAATCTTGAAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTC 500
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501 TTATTTCACTGAATCTGAAAGTGAGGGAATTTGTTGCCACGATATACAGAAACTTTAGG 560
362 TTATTTGACCTGATGCTCGACGCTCAATACAAACTGGTGCATGATGATTAACAGGCTTAAG 421
561 CGAAGTATGAGACATACAAAATGTCAACAG 593
422 CTAAATTTGAGCTTTTGGAGAGAACCAAGAGC 454

RESULT 3
US-09-853-450-3
; Sequence 3, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:

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1  APPLICANT: Yanofsky, Martin F.
2  APPLICANT: Pelaz, Soraya
3  APPLICANT: Dilta, Gary
4  APPLICANT: The Regents of the University of California
5  TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
6  TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
7  FILE REFERENCE: 19452A-002400US
8  CURRENT APPLICATION NUMBER: US/09/853,450
9  CURRENT FILING DATE: 2001-05-03
10 NUMBER OF SEQ ID NOS: 61
11 SOFTWARE: PatentIn Ver. 2.1
12 SEQ ID NO: 3
13 LENGTH: 794
14 TYPE: DNA
15 ORGANISM: Brassica oleracea
16 FEATURE:
17 NAME/KEY: CDS
18 LOCATION: (36)..(794)
19 OTHER INFORMATION: APETALAI (Ap1)
20 US-09-853-450-3

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Query March 26.7%; Score 158.6; DB 9; Length 794;
Best Local Similarity 67.3%; Pred. No. 1.6e-40;
Matches 224; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

Dy 261 ATATGGGTCCGGCGAAGGTGCAGCTGAAAGCGGATAGAGAACAGATTAATCGGAGGTGA 320
Db 34 AAATGGGAAGGGGATAGGGTTCAATTGGAAGGATAGAAAAACAAGTCAATAGACAAGTGA 93
Dy 321 CCTTCTCCAAAGCGCCGCAACGGGCTCCTGAAAGAAAGCGCAGAGTCTCCGCTCTGTG 380
Db 94 CATTCGAAAGAAAGAGCTGTGTCTTATGAAAGAAAGCTCATGAGATCTCTTCTGTGTG 153
Dy 381 ACGGGAGAGTCCCGGTATCGTCTTCCGCCCAAGGCAAGCTCATGAGTAGCGCACCG 440
Db 154 ATGCTGAAGTTGGCGCTGTGTCTTCTCCATTAAGGGGAAACTCTTAAATATCTCAGTG 213
Dy 441 ACTCCAGCATGAGCAAAATCTTAAAGCTTATGAGCGCTACTCTTATCTGAAAGGCTC 500
Db 214 ATCTCTGATGAGAAAGTACTTTAGACCTATGAGAGTACTCTTAGCCCGAGACAGCG 273
Dy 501 TTATTTGAGTGAATCTGMAAGTAGAGGAAATTGGTGCACGAATACAGAGAACTTAAAG 560
Db 274 TTATAGACCTGAGAGTCGAGTCCAAATACGAAGTGGTCATGAGATATATAGGCTTAAAG 333
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Db 334 CTAAGATTGAGCTTTTGGAGAGAAAAACGAGAGGC 366

RESULT 4
US-09-978-729A-1
; Sequence 1, Application US/09978729A
; Patent No. US20020178465A1
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Martin F.
; APPLICANT: Liljegen, Sarah
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000950US
; CURRENT APPLICATION NUMBER: US/09/978, 729A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Arabidopsis sp.

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Qy	252	GAATATGAGTATATGGTCCGGCGCAAGTGTGCACTGAACGGATAGAGAAACAAGTAAATC	311
Db	138	GCAACAAGCGCATGGGGCGCCGCCAAGTACAGCTGAACGGATAGAGAACAAAGTTAAACC	197
Qy	312	GGAGGTGACCTTTCCAAGCGCCGCATCGGGCTCTGAAGAGCGCAGAGTCTCCG	371
Db	198	GGCAGGTGACCTTCTCCAAAGCGCCGGAACGGCGTCTCAAGAGCGCAGCAGATCTCCG	257
Qy	372	TCTCTGTACGCGGAGGTCCGCCCTCATCGTCTTCTCCCGCAAGGCAAGCTCTATAGT	431
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QY 381 ACGGAGAGTGGCCGTCATGCTTCTTCCCAAGGCAAGCTTATAGTACGCCACCG 440
DB 154 ATGCTGAAGTGGCGCTGTGTCTTCTCCCAATAGGGGAACTTTGAATCTCCACTG 213
QY 441 ACTCAGATGAGCAAAATCTTGAAGCTTATAGCGCTACTCTTATGCTGAAAAGGCTC 500
DB 214 ATCTCTGTATGAGAGAACTTGTAGACGCTATGAGAACTTACCGCCGAGAGACAGC 273
QY 501 TTATTTAGCTGAATCTGAAAGTGAAGGAAATGCTGCGCAATATACAGAACTTAAG 560
DB 274 TTATAGCACTGAGCTGAGCTGCACTCCATATAGAACTGTGATGAGATATATAGCTTAAG 333
QY 561 CGAAGATTGAGACCATACAAAATGTCAAGC 593
DB 334 CTAAGATTGAGCTTTTGGAGAGAAACCAAGGC 366

RESULT 15

US-08-659-188-3

Sequence 3, Application US/08659188

Patent No. 6002069

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 36..794
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..794
OTHER INFORMATION: /note= "product = Brassica oleracea
OTHER INFORMATION: APl."
US-08-659-188-3

Query Match

26.7%; Score 158.6; DB 3; Length 794;

Best Local Similarity 67.3%; Pred. No. 4e-35;

Matches 224; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

DB 34 AAATGGAGGGGTAGGGTTCACTTGAAGAGATAGAAAACAAGATCAATACAGACGTGA 93
QY 321 CTTTCTCCAAAGCGCGCAACGGCTCCTGAAGAGCGCACAGATCTCCGCTCTGTG 380
DB 94 CATTCTGAAAAGAGAGCTGTCTTATGAAAGAACTCATGATCTCTGTCTGTG 153
QY 381 ACGGAGAGTGGCCGTCATGCTTCTTCCCAAGGCAAGCTTATAGTACGCCACCG 440
DB 154 ATGCTGAAGTGGCGCTGTGTCTTCTCCCAATAGGGGAACTTTGAATCTCCACTG 213
QY 441 ACTCAGATGAGCAAAATCTTGAAGCTTATAGCGCTACTCTTATGCTGAAAAGGCTC 500
DB 214 ATCTCTGTATGAGAGAACTTGTAGACGCTATGAGAACTTACCGCCGAGAGACAGC 273
QY 501 TTATTTAGCTGAATCTGAAAGTGAAGGAAATGCTGCGCAATATACAGAACTTAAG 560
DB 274 TTATAGCACTGAGCTGAGCTGCACTCCATATAGAACTGTGATGAGATATATAGCTTAAG 333
QY 561 CGAAGATTGAGACCATACAAAATGTCAAGC 593
DB 334 CTAAGATTGAGCTTTTGGAGAGAAACCAAGGC 366

Search completed: June 29, 2003, 07:26:47

Job time : 36 secs

Oy	561	CGAAGATTGAGACCATACAAAATGTCACAAAGC	5933
Db	439	CTAAGATTGAGCTTTTGGAGAGAAACGAGAGGC	4711

RESULT 13

US-09-149-976-1
Sequence 1, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
FILE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: join(141..905, 909..971, 975..1047)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1215
OTHER INFORMATION: /note="product = Arabidopsis
thaliana Api"
US-09-149-976-1

Query Match	27.6%	Score 163.4;	DB 3;	Length 1215;
Best Local Similarity	68.2%	Pred. No. 2.2e-36;		
Matches 227; Conservative	0;	Mismatches 106;	Indels 0;	Gaps 0

QY 261 AATATGGGTCCGGCAAGTGCAGCTCTAAGCGGATAGAGAAACAAGATTAATCCGACAGTGA 320
Db 139 AATATGGGAAGGGTATGGCTTCAATTAGAGAGATAGAGAACCAAGATCAATAGACAACTGA 198
QY 321 CTTTCTTCCAAGCGCCCAACGGGCTCCTGAAGAAGCGCACAGATCTCCGTCTCTGTG 380
Db 199 CATTTCTGAAAAGAAAGACTGCTGTTTTGAAGAAAGCTCAATGAGATCTCTGTTCTCTGTG 258
QY 381 ACGCGAGGTCCGCGTCATCTGCTTCTCCCCCAAGAAGCAAGCTTATAGTAGACCCACCG 440
Db 259 ATGCTGAAAGTGTCTTGTTGTCTCTCCCATTAAGGAAAACTTTCGAATACTCCACTG 318

QY 444 ACCTCAGCAGTGGCAAAATCTTGAACGTTATGACCGCTACTTATGCTGAAGAAGCTC 500
 Db 319 ATTCTGTATGGGAAGATACCTTGAACGTTATGAAGGACTCTTACCCGAAAGACAGC 378
 QY 501 TTATTCAGCTGAATCTGGAAGTGAGGGAATTTGGTCCACGATATACGAAACTTAAG 566
 Db 379 TTATTCACCTGTGCTCGACGTCATACAAATGGATCATGAGATATACAGGCTTAAG 438
 QY 561 CGAAGATTGAGCCATACAAAATGTCACAGC 593
 Db 439 CTAAAGATTAGCTTTGGAGAGAAACCGAGGC 471

RESULT 14

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US-08-592-214A-3
Sequence 3, Application US/08592214A
Patent No. 581536
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 794 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 36..794
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..754
OTHER INFORMATION: /note= "product = Brassica oleracea
US-08-592-214A-3

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Query Match	26.7%	Score 158.6	DB 1	Length 794
Best Local Similarity	67.3%	Pred. No. 46-35		
Matches 224	Conservative	0	Mismatches 109	Indels 0
				Gaps 0

QY 2 61 AATAGGTCGGCCGAAGGTCAGCTGAGGCGATTGAGAAACAAGATAAATTCGCACTGA 320
Db 34 AATATGGAAAGGGTATGGGTTCACTTGTAGACGATACAAAAACAAGATCAATAGACAACTGA 93
QY 321 CCTTCTCCAAAGCCGCCAAGGAGCTCTCTGAAGAGGCGACAGATCTCCGTCCTCTGTG 380
Db 94 CATTCCTCGAAAGAAGAGCTGCTCTTATATGAACAAAGCTCATGAGATCTCTGTTCTGTG 153

TITLE OF INVENTION: Reproductive Development and Methods of Making Same
US-08-592-214A-1
SEQUENCE 1, Application US/08592214A
Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Vanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-09-398-326-1

Query Match 27.6%; Score 163.4; DB 4; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGTCGCGGCAAGTGTGAGCGGATGAGACAAATTAATCGCGAGGTGA 320
122 AATGGGAAGGGGTGAGGTTCAATTGAGAGGATGAGAACAAATAGACAAAGTGA 181
321 CCTTCCAGGCGCGCAAGGGCTCTGAAAGGCGGACGAGATCTCCGCTCTGTG 380
182 CATTTTCGAAAGAAAGAGCTGTCTTTGAGAAAGAGCTATAGATCTGTCTGTG 241
381 ACGGAGAGTCCCGCTCATCGTCTTCTCCCAAGGCAAGCTATAGTACGCCACG 440
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302 ATTTCTTATGAGAGAAATTAATGAAAGCTATGAGAGGTAAGCTTACCGCAAGACAGC 361
501 TTATTTGAGTGAATCTGAAGTGAAGGAAATTTGTGCGCAAGATACAGAAACTTAAG 560
362 TTATTTGACCTGAGTCCGAGCTCAATACAAAGTGTGATGAGTAAACAGCTTAAG 421
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422 CTAGATTGAGCTTTTGGAGAGAAACAGAGGC 454

RESULT 12
US-08-592-214A-1
SEQUENCE 1, Application US/08592214A
Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Vanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: join(141..905, 909..971, 975..1047)
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1215
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-08-592-214A-1

Query Match 27.6%; Score 163.4; DB 1; Length 1215;
Best Local Similarity 68.2%; Pred. No. 2.2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGTCGCGGCAAGTGTGAGCGGATGAGACAAATTAATCGCGAGGTGA 320
139 AATGGGAAGGGGTGAGGTTCAATTGAGAGGATGAGAACAAATAGACAAAGTGA 198
321 CCTTCCAGGCGCGCAAGGGCTCTGAAAGGCGGACGAGATCTCCGCTCTGTG 380
199 CATTTTCGAAAGAAAGAGCTGTCTTTGAGAAAGAGCTATGAGATCTGTCTGTG 258
381 ACGGAGAGTCCCGCTCATCGTCTTCTCCCAAGGCAAGCTATAGTACGCCACG 440
259 ATGCTGAAGTGTCTGTGTCTCTCTCCCAAGGGAAGTCTTCAATCTCACTG 318
441 ACTCAGATGAGCAAAATTTCTTGAAGCTTATGAGCGCTACTTATGCTGAAAAGCTC 500
319 ATTTCTTATGAGAGAAATTAATGAAAGCTATGAGAGGTAAGCTTACCGCAAGACAGC 378
501 TTATTTGAGTGAATCTGAAGTGAAGGAAATTTGTGCGCAAGATACAGAAACTTAAG 560
379 TTATTTGACCTGAGTCCGAGCTCAATACAAAGTGTGATGAGTAAACAGCTTAAG 438

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-08-655-227-1

Query Match 27.6%; Score 163.4; DB 3; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
DB 261 ATATGGTCGCGGCAAGGTGACGTGAAGCGGATAGAGAAACAATTAATCGGAGGTGA 320
122 AAATGGGAAGGGGTAGGGTTCATTGAAAGAGATAGAGAAAGATCAATAGACAGTGA 181
QY 331 CTTTCTCCAGAGCGCGCAACGGGCTCTGAAAGAGCGGACAGATCTTCCTCTGTG 380
182 CATCTCGAAAGAGAGAGGTGCTTTTGAAGAAAGCTCATGATCTCTGTCTGTG 241
DB 381 ACGGAGAGTGGCGGTCACTCTCTCTCCCAAGGCAAGCTCTATGAGTACGCCACG 440
242 ATGCTGAAGTGTCTCTGTCTCTCTCCATAGGGGAACTCTTCGAAATCTCCACTG 301
QY 441 ACTCAGCATGACAAATTTCTGAACGTTATGAGCGCTACTTATGCTGAAGAGCTC 500
302 ATTCTGTATGAGAAAGATCTTGAACGCTATGAGAGGTACTCTTAAGCGCGAAGACAC 361
DB 501 TTATTTAGCTGAATCTGAAAGTGAAGGAAATTGCTGCCAGATACAGAAACTTAAG 560
362 TTATTTAGCACTGAGTCCGACGTCAATACAACTGGTGCATGAGATATACAGGCTTAAG 421
QY 561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
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RESULT 10
US-08-655-241-1
Sequence 1, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigelt, Detlef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
NUMBER OF SEQUENCES: 26
DEVELOPMENT AND METHODS OF MAKING SAME
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note= "product = Arabidopsis
OTHER INFORMATION: thaliana Apl."
US-08-655-241-1

Query Match 27.6%; Score 163.4; DB 3; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;
DB 261 ATATGGTCGCGGCAAGGTGACGTGAAGCGGATAGAGAAACAATTAATCGGAGGTGA 320
122 AAATGGGAAGGGGTAGGGTTCATTGAAAGAGATAGAGAAAGATCAATAGACAGTGA 181
QY 331 CTTTCTCCAGAGCGCGCAACGGGCTCTGAAAGAGCGGACAGATCTTCCTCTGTG 380
182 CATCTCGAAAGAGAGGTGCTTTTGAAGAAAGCTCATGATCTCTGTCTGTG 241
DB 381 ACGGAGAGTGGCGGTCACTCTCTCTCCCAAGGCAAGCTCTATGAGTACGCCACG 440
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DB 501 TTATTTAGCTGAATCTGAAAGTGAAGGAAATTGCTGCCAGATACAGAAACTTAAG 560
362 TTATTTAGCACTGAGTCCGACGTCAATACAACTGGTGCATGAGATATACAGGCTTAAG 421
QY 561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
422 CTAAGATTGAGCTTTTGGAGAGAAACCAAGAGC 454
DB

RESULT 11
US-09-398-326-1
Sequence 1, Application US/09398326
Patent No. 635863
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early

OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,156
FILING DATE: 12-21-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,336
FILING DATE: 12-21-94
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/013001
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1054
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-576-156-1

Query Match 27.6%; Score 163.4; DB 2; Length 1054;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGTGGCGGCAAGTGTGACGATGAGAGCAAGATTAATCGGAGGTGA 320
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321 CTTCTCCAGGCGCGCAAGGGCTCTGAGAGAGCGACAGATCTCTCTGTG 380
182 CATTCGAAAGAGAGAGCTGTCTTTGAAGAAAGCTATAGATCTCTCTGTG 241
381 ACGGAGAGTGGCCGTCATGCTCTCTCCCAAGAGCAAGCTATAGAGTACGCG 440
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441 ACTCAGATGAGCAAAATTTCTGAACGTTATGAGCGCTACTCTTATGTGAAGGCTC 500
302 ATCTTGATGAGAGAGATCTTGAACGCTATGAGAGGATCTTACCGCGAAAGACAGC 361
501 TTATTTAGCTGAATCTGAAAGTGAAGGAATTGGTCCACGAAATACAGAACTTAAAG 560
362 TTATTTGACCTGAGTCCGACGTCATACAACTGGTGCATGAGATTAACAGGCTTAAAG 421
561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
422 CTAAGATTGAGCTTTTGGAGAGAAACCAAGAGC 454

RESULT 8
US-08-659-188-1
Sequence 1, Application US/08659188
Patent No. 6002069

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 124..893
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1057
OTHER INFORMATION: /note="product = Arabidopsis
OTHER INFORMATION: thaliana API."
US-08-659-188-1

Query Match 27.6%; Score 163.4; DB 3; Length 1057;
Best Local Similarity 68.2%; Pred. No. 2e-36;
Matches 227; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

261 ATATGGTGGCGGCAAGTGTGACGATGAGAGCAAGATTAATCGGAGGTGA 320
122 AATGGAAGGGGTAGGGTTCAATGAGAGATGAGAAAGATCAATAGCAAGTGA 181
321 CTTCTCCAGGCGCGCAAGGGCTCTGAGAGAGCGACAGATCTCTCTGTG 380
182 CATTCGAAAGAGAGAGCTGTCTTTGAAGAAAGCTATGAGATCTCTCTGTG 241
381 ACGGAGAGTGGCCGTCATGCTCTCTCCCAAGGCAAGCTTATGAGTACGCG 440
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501 TTATTTAGCTGAATCTGAAAGTGAAGGAATTGGTCCACGAAATACAGAACTTAAAG 560
362 TTATTTGACCTGAGTCCGACGTCATACAACTGGTGCATGAGATTAACAGGCTTAAAG 421
561 CGAAGATTGAGACCATACAAAATGTCAACAGC 593
422 CTAAGATTGAGCTTTTGGAGAGAAACCAAGAGC 454

RESULT 9
US-08-655-227-1
Sequence 1, Application US/08655227
Patent No. 6025483

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APTALAI Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays APL"
US-09-149-976-7

Query Match: 50.7%; Score 300.4; DB 3; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAATCAGATATGGGTGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 311
DB 138 GCAACAGGCGATGGGGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 197
QY 312 GCGAGTACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 371
DB 198 GCGAGTACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 257
QY 372 TCCTGTGAGCGGAGGTGCGCGTCAATGCTTCTCCCGCAAGCGCTATGAGT 431
DB 258 TCCTGTGAGCGGAGGTGCGCGTCAATGCTTCTCCCGCAAGCGCTATGAGT 317
QY 432 ACGCCACGACTCCGATGAGCAAAATCTTGAAGCGCTACTTATGCTG 491
DB 318 ACGCCACGACTCCGATGAGCAAAATCTTGAAGCGCTACTTATGCTG 377
QY 492 AAAAGCTCTTATTTCACTGAAATCTGAAAGTGAAGGAAATGTCGCAATACAGA 551
DB 378 AAAAGCTCTTATTTCACTGAAATCTGAAAGTGAAGGAAATGTCGCAATACAGA 437
QY 552 AACTTAAGGCGAAGTGAAGCAATACAAATATGTCACAGC 593
DB 438 AACTTAAGGCGAAGTGAAGCAATACAAATATGTCACAGC 479

RESULT 6

US-09-398-326-7
Sequence 7, Application US/09398326
Patent No. 6355863

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/398,326
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/659,188
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays APL."
US-09-398-326-7

Query Match: 50.7%; Score 300.4; DB 4; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 252 GAATCAGATATGGGTGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 311
DB 138 GCAACAGGCGATGGGGCGCGCAAGTGCAGCTGAGCGGATGAGAACAGATTAATC 197
QY 312 GCGAGTACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 371
DB 198 GCGAGTACCTTCTCCAAAGCGCGCAAGCGGCTCTGAGAAAGCGCGAGATCTCG 257
QY 372 TCCTGTGAGCGGAGGTGCGCGTCAATGCTTCTCCCGCAAGCGCTATGAGT 431
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QY 432 ACGCCACGACTCCGATGAGCAAAATCTTGAAGCGCTACTTATGCTG 491
DB 318 ACGCCACGACTCCGATGAGCAAAATCTTGAAGCGCTACTTATGCTG 377
QY 492 AAAAGCTCTTATTTCACTGAAATCTGAAAGTGAAGGAAATGTCGCAATACAGA 551
DB 378 AAAAGCTCTTATTTCACTGAAATCTGAAAGTGAAGGAAATGTCGCAATACAGA 437
QY 552 AACTTAAGGCGAAGTGAAGCAATACAAATATGTCACAGC 593
DB 438 AACTTAAGGCGAAGTGAAGCAATACAAATATGTCACAGC 479

RESULT 7

US-08-576-156-1
Sequence 1, Application US/08576156
Patent No. 5844119

GENERAL INFORMATION:

APPLICANT: Weigelt, Detlef
TITLE OF INVENTION: Genetically Modified Plants Having Modulated
TITLE OF INVENTION: Flower Development
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..1345
OTHER INFORMATION: /note= "product = Zea mays APL."
US-08-655-227-7

Query Match 50.7%; Score 300.4; DB 3; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 252 GAAATCAGATATATGATGCGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAAATTAATC 311
Db 138 GCAACAGGCGATGGGCGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAAATTAATC 197
Qy 312 GCGAGTGACCTTCTCCAAAGCGCGCAACGGGCTCTTGAAGAGCGGCAAGATCTCG 371
Db 198 GCGAGTGACCTTCTCCAAAGCGCGGCAACGGGCTCTTGAAGAGCGGCAAGATCTCG 257
Qy 372 TCCTGTGAGCGGAGGTGCGCGCTCATCTTCTTCCCGCAAGCGGCAAGCTCTATGAGT 431
Db 258 TCCTGTGAGCGGAGGTGCGCGCTCATCTTCTTCCCGCAAGCGGCAAGCTCTATGAGT 317
Qy 432 AGCGCAGCATCTCCAGCATGAGCAAAATTTGAAAGTTATGAGCGCTACTTATGCTG 491
Db 318 AGCGCAGCATCTCCCGCATGAGCAAAATTTGAAAGTTATGAGCGCTACTTATGCTG 377
Qy 492 AAAAGCTCTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGTCGACGATACAGA 551
Db 378 AAAAGCTCTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGTCGACGATACAGA 437
Qy 552 AACTTAAGCGGAGATTTGAGACCATACAAAATTTGTCACAGC 593
Db 438 AACTGAAGGCCAAATTTGAGACCATACAAAATTTGTCACAGC 479

RESULT 4

US-08-655-241-7
Sequence 7, Application US/08655241
Patent No. 6025543

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

APPLICANT: Weigel, Detlef

TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive

TITLE OF INVENTION: Development and Methods of Making Same

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/655,241

FILING DATE: 05-JUN-1996

CLASSIFICATION: CLASS 800

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 1894

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1345 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 149..968

Query Match 50.7%; Score 300.4; DB 3; Length 1345;
Best Local Similarity 92.4%; Pred. No. 1.3e-74;
Matches 316; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 252 GAAATCAGATATATGATGCGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAAATTAATC 311
Db 138 GCAACAGGCGATGGGCGCGGCAAGTGCAGCTGAAGCGGATAGAGAACAAATTAATC 197
Qy 312 GCGAGTGACCTTCTCCAAAGCGCGCAACGGGCTCTTGAAGAGCGGCAAGATCTCG 371
Db 198 GCGAGTGACCTTCTCCAAAGCGCGGCAACGGGCTCTTGAAGAGCGGCAAGATCTCG 257
Qy 372 TCCTGTGAGCGGAGGTGCGCGCTCATCTTCTTCCCGCAAGCGGCAAGCTCTATGAGT 431
Db 258 TCCTGTGAGCGGAGGTGCGCGCTCATCTTCTTCCCGCAAGCGGCAAGCTCTATGAGT 317
Qy 432 AGCGCAGCATCTCCAGCATGAGCAAAATTTGAAAGTTATGAGCGCTACTTATGCTG 491
Db 318 AGCGCAGCATCTCCCGCATGAGCAAAATTTGAAAGTTATGAGCGCTACTTATGCTG 377
Qy 492 AAAAGCTCTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGTCGACGATACAGA 551
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Qy 552 AACTTAAGCGGAGATTTGAGACCATACAAAATTTGTCACAGC 593
Db 438 AACTGAAGGCCAAATTTGAGACCATACAAAATTTGTCACAGC 479

RESULT 5

US-09-149-976-7
Sequence 7, Application US/09149976
Patent No. 6127123

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Cauliflower Floral Meristem Identity

TITLE OF INVENTION: Genes and Methods of Using Same

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/149,976

FILING DATE: 09-SEP-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/592,214

FILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3291

TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2003, 07:25:59 ; Search time 1068 Seconds
(without alignments)
8992.438 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 593

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Optimal number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	421.8	71.1	567 13	BJ207882 BJ207882
3	421.4	71.1	716 13	BJ304647 BJ304647
4	402	67.8	492 10	BE500707 BE500707
5	395.2	66.6	555 12	BG605208 WHE2330_A
6	394.8	66.6	691 13	BJ316394 BJ316394

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9	385.4	65.0	1568 13	BI956235
10	384.4	64.8	551 10	BE498620
11	360.8	60.8	622 13	BI957545
12	325	54.8	623 13	BI957545
13	304	51.3	572 14	BI957545
14	290.4	49.0	1488 11	BI957545
15	280	47.2	486 12	BI957545
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ALIGNMENTS

RESULT 1
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DEFINITION BJ208073 Y. Ogihara unpublished cDNA library, wh Triticum aestivum
CDNA clone wh6110 5', mRNA sequence.
ACCESSION BJ208073
VERSION BJ208073.1 GI:19946124
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; Poideae
; Triticaceae; Triticum.
REFERENCE
1 (bases 1 to 633)
Ogihara, Y. and Mural, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
CONTACT: Tadashi Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES

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/cultivar="Chinese Spring"
/db_xref="taxon:4565"

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/clone_type="spike at meiosis"
/dev_stage="Peekes" scale 9"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pluscript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

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BASE COUNT 171 a 189 c 151 g 122 t

Query Match 86.7%; Score 514.2; DB 13; Length 633;
Best Local Similarity 99.4%; Pred. No. 1.4e-122;

Matches 516; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 361 CCACGAGCTCCAGATGACAAATTTCTTGAAGCTTATGAGCGCTACTCTTATGCTGAA 420
OY 495 AGGTCTTATTTCACTGATCTGAAAGTGAAGGAAATTTGTCACGAAATACAGAAAC 554
DB 421 AGGTCTTATTTCACTGATCTGAAAGTGAAGGAAATTTGTCACGAAATACAGAAAC 480
OY 555 TTAAGCGAAGATTGAGACCAATACAAAATGTCCACAAGC 593
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LOCUS BJ207882 567 bp mRNA linear EST 04-APR-2002
DEFINITION BJ207882 Y. Ogiwara unpublished cDNA library, Wh Triticum aestivum
cDNA clone whsm21 5', mRNA sequence.
ACCESSION BJ207882
VERSION BJ207882.1 GI:19945861
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae

REFERENCE
1 (bases 1 to 567)
Ogiwara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
JOURNAL
Contact: Tadashi Shin-1
Center for Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.

FEATURES
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone_lib="whsm21"
/clone_type="spike at meiosis"
/dev_stage="Peekes" scale 9"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pluscript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 157 a 155 c 147 g 108 t

Query Match 71.1%; Score 421.8; DB 13; Length 567;
Best Local Similarity 99.1%; Pred. No. 1.2e-98;

Matches 435; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

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OY 155 ATCTCCCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 214
DB 1 ATCTCCCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
OY 215 TCGCGCGCATGACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 274
DB 61 TCGCGCGCATGACAAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118
OY 275 AAGGTGAGCTGAGAGCGATGAGAAATTAATCGGCGAGTGAACCTTCTCCAAAGCGC 334
DB 119 AAGGTGAGCTGAGAGCGATGAGAAATTAATCGGCGAGTGAACCTTCTCCAAAGCGC 178
OY 335 CGCAACGGGCTCTGAAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
DB 179 CGCAACGGGCTCTGAAAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 238
OY 395 GTCAATGCTTCTCTCCCAAGGCAAGTCTATAGTACGCAACGACTCCAGATGAGC 454
DB 239 GTCAATGCTTCTCTCCCAAGGCAAGTCTATAGTACGCAACGACTCCAGATGAGC 298
OY 455 AAAATTTCTTGAAGCTTATGAGCGCTACTCTATGCTGAAAGGCTTATTTAGCTGAA 514
DB 299 AAAATTTCTTGAAGCTTATGAGCGCTACTCTATGCTGAAAGGCTTATTTAGCTGAA 358
OY 515 TCTGAAAGTGAAGAAATTTGCTGCGCAGCAATACAGAAATTTAAAGCGGAGATTGAGAC 574
DB 359 TCTGAAAGTGAAGAAATTTGCTGCGCAGCAATACAGAAATTTAAAGCGGAGATTGAGAC 418
OY 575 ATACAAAATGTCCACAAGC 593
DB 419 ATACAAAATGTCCACAAGC 437

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RESULT 3
BJ304647 716 bp mRNA linear EST 09-APR-2002
LOCUS BJ304647
DEFINITION BJ304647 Y. Ogihara unpublished cDNA library, Wh_yd Triticum
aestivum cDNA clone whyd7c05 5', mRNA sequence.
ACCESSION BJ304647
VERSION BJ304647.1 GI:20114624
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
1 (bases 1 to 716)
REFERENCE Ogihara,Y. and Murai,K.
1 (bases 1 to 716)
TITLE Expressed genes in Triticum aestivum
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1. 716
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone_1db="Y. Ogihara unpublished cDNA library, Wh_yd"
/clone_1db="whyd7c05"
/tissue_type="spikelet at late flowering"
/dev_stage="Feekes' scale 6"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pluescript phagemids in the TV Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 210 a 190 c 200 g 116 t
ORIGIN
Query Match 71.1%; Score 421.4; DB 13; Length 716;
Best Local Similarity 99.3%; Pred. No. 1.6e-98;
Matches 43; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
QY 157 CTCCCTACCGCGCGCGGAGCGAGCAGCTCTGCTCTCCACCCCGCGCGGTG 216
DB 20 CTCCCTACCGCGCGCGCGGAGCGAGCAGCTCTGCTCTCCACCCCGCGCGGTG 79
QY 217 CGCGCATTAGACAAAGAGCGGAGCAGCTAGTCCGGAATAGATATGGTCCGCGAA 276
DB 80 CGGCCATTAGACAAAGAGCGGAGCAGCTAGTCCGGAATAGAGG-ATGGGTCCGCGCAA 137
QY 277 GGTCACGTGAAGCGGATAGAGAACAGATTAATCGAGGTGACCTTCTCCAGCGCGG 336
DB 138 GGTCACGTGAAGCGGATAGAGAACAGATTAATCGAGGTGACCTTCTCCAGCGCGG 197
QY 337 CAAGGAGCTCTGAAGAGCGGAGCAGATCTCCGCTCTGTGACGCGAGGTGCGCGT 396
DB 198 CAAGGAGCTCTGAAGAGCGGAGCAGATCTCCGCTCTGTGACGCGAGGTGCGCGT 257
QY 397 CATGCTCTTCTCCCGCAAGGAGCAGCTTATGATGAGCCAGCGAGCTTCAGCATGACAA 456
DB 258 CATGCTCTTCTCCCGCAAGGAGCAGCTTATGATGAGCCAGCGAGCTTCAGCATGACAA 317

QY 457 AATCTTGAAGCTTATGAGCGCTACTTATGCTGAAGAGCTTATTTACGCTGATC 516
DB 318 AATCTTGAAGCTTATGAGCGCTACTTATGCTGAAGAGCTTATTTACGCTGATC 377
QY 517 TGAAGTGAAGAAATTTGGTCCAGCAATACAGAACTTAAAGCGGAATGAGCAAT 576
DB 378 TGAAGTGAAGAAATTTGGTCCAGCAATACAGAACTTAAAGCGGAATGAGCAAT 437
QY 577 ACAAAATGTCACAGC 593
DB 438 ACAAAATGTCACAGC 454

RESULT 4
BE500707 492 bp mRNA linear EST 04-AUG-2000
LOCUS BE500707
DEFINITION WHE0991-0994_121_121S wheat pre-anthesis spike cDNA library
Triticum aestivum cDNA clone WHE0991-0994_121_121, mRNA sequence.
ACCESSION BE500707
VERSION BE500707.1 GI:9699324
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticaceae; Triticum.
1 (bases 1 to 492)
REFERENCE Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hala,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C:
The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: anders@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1. 492
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone_1db="WHE0991-0994_121_121"
/clone_1db="wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pluescript
phagemids in the TV Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 140 a 131 c 128 g 93 t
ORIGIN
Query Match 67.8%; Score 402; DB 10; Length 492;
Best Local Similarity 99.8%; Pred. No. 1.5e-93;
Matches 41; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 180 CAGCAGCTCTGCTCTCCACCCCGCGCGGTGCGGCGCATGACAAAGAGCGGA 239

Db 2 CAGGACGCTCTGCGCTCTCC-CCCCGCGCGCGCCGATAGACACAGAGCCGA 60

Qy 240 CAGTATATGCGCAATATAGATATGCTCCGCGAAGCTGACGTGAAGGATAGAGA 299

Db 61 CAGCTAGATCGCGAAATCAGATATGCTCCGCGAAGCTGACGTGAAGGATAGAGA 120

Qy 300 ACAAGATTAATCGCGAGGTGACCTTCTCCAGCCGCGCAAGGCTCTCTGAAGAGCGC 359

Db 121 ACAAGATTAATCGCGAGGTGACCTTCTCCAGCCGCGCAAGGCTCTCTGAAGAGCGC 180

Qy 360 ACGAGATCTCCGCTCTCTGTGACGCGAGGTGCGCGCTGATCTTCTTCCCAAGGCA 419

Db 181 ACGAGATCTCCGCTCTCTGTGACGCGAGGTGCGCGCTGATCTTCTTCCCAAGGCA 240

Qy 420 AGCTTATGATAGCGCCACCGATCTCCAGATGACCAAAATCTTGAAGTATAGAGCT 479

Db 241 AGCTTATGATAGCGCCACCGATCTCCAGATGACCAAAATCTTGAAGTATAGAGCT 300

Qy 480 ACTCTTATGCTGAAAAGGCTCTTATTTGAGCTGATCTGAAGTGAAGAAATTTGTCGC 539

Db 301 ACTCTTATGCTGAAAAGGCTCTTATTTGAGCTGATCTGAAGTGAAGAAATTTGTCGC 360

Qy 540 ACGAATACAGAACTTAAGCGCAAGATTGAGACCATACAAAATGTCAAGC 593

Db 361 ACGAATACAGAACTTAAGCGCAAGATTGAGACCATACAAAATGTCAAGC 414

RESULT 5 555 bp mRNA linear EST 16-APR-2001
Bg605208
LOCUS
DEFINITION
WH2330_A04_A0825 wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WH2330_A04_A08, mRNA sequence.
Bg605208
Bg605208.1 GI:13635211
EST.
SOURCE
broad wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE
AUTHORS
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rauech, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genome - Pre-anthesis spike cDNA library
Unpublished (2000)
JOURNAL
COMMENT
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@wp.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
FEATURES
source
Location/Qualifiers
1..555
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WH2330_A04_A08"
/clone_lib="wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="vector: lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI, Site 2: XhoI; plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pluescript

BASE COUNT 161 a 143 c 147 g 104 t

ORIGIN

Query Match 66.6%; Score 395.2; DB 12; Length 555;
Best Local Similarity 98.8%; Pred. No. 8.8e-92;
Matches 409; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 180 CAGGACGCTCTGCGCTCTCTCCACCCGCGCGCGCGCCATAGACCAAGAGCCGA 239

Db 1 CAGGACGCTCTGCGCTCTCTCCACCCGCGCGCGCGCCATAGACCAAGAGCCGA 60

Qy 240 CAGTATATGCGCAATATAGATATGCTCCGCGAAGCTGACGTGAAGGATAGAGA 299

Db 61 CAGCTAGATCGCGAAATCAGATATGCTCCGCGAAGCTGACGTGAAGGATAGAGA 118

Qy 300 ACAAGATTAATCGCGAGGTGACCTTCTCCAGCCGCGCAAGGCTCTCTGAAGAGCGC 359

Db 119 ACAAGATTAATCGCGAGGTGACCTTCTCCAGCCGCGCAAGGCTCTCTGAAGAGCGC 178

Qy 360 ACGAGATCTCCGCTCTCTGTGACGCGAGGTGCGCGCTGATCTTCTTCCCAAGGCA 419

Db 179 ACGAGATCTCCGCTCTCTGTGACGCGAGGTGCGCGCTGATCTTCTTCCCAAGGCA 238

Qy 420 AGCTTATGATAGCGCCACCGATCTCCAGATGACCAAAATCTTGAAGTATAGAGCT 479

Db 239 AGCTTATGATAGCGCCACCGATCTCCAGATGACCAAAATCTTGAAGTATAGAGCT 298

Qy 480 ACTCTTATGCTGAAAAGGCTCTTATTTGAGCTGATCTGAAGTGAAGAAATTTGTCGC 539

Db 299 ACTCTTATGCTGAAAAGGCTCTTATTTGAGCTGATCTGAAGTGAAGAAATTTGTCGC 358

Qy 540 ACGAATACAGAACTTAAGCGCAAGATTGAGACCATACAAAATGTCAAGC 593

Db 359 ACGAATACAGAACTTAAGCGCAAGATTGAGACCATACAAAATGTCAAGC 412

RESULT 6 691 bp mRNA linear EST 09-APR-2002
Bj316394
LOCUS
DEFINITION
Bj316394 Y. Ogihara unpublished cDNA library, wh_yf Triticum
aestivum cDNA clone wh_yf22009 5', mRNA sequence.
Bj316394
Bj316394.1 GI:20121662
EST.
SOURCE
broad wheat.
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE
AUTHORS
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
JOURNAL
COMMENT
Contact: Tadashi Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tehin@genes.nig.ac.jp.
FEATURES
source
Location/Qualifiers
1..691
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whyf22009"
/clone_lib="Y. Ogihara unpublished cDNA library, wh_yf"
/tissue_type="spikelet at early flowering"
/dev_stage="Peekes' scale 6"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid phagemids in the T7 Close Lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 210 a 179 c 189 g 113 t
ORIGIN

Query Match 66.6%; Score 394.8; DB 13; Length 691;
Best Local Similarity 99.0%; Pred. No. 1.2e-91;
Matches 408; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

182 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAAGAGCCGACA 241
2 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAAGAGCCGACA 61
242 GCTAGATCGCGAAATCAGATATGGTGGCGGCAAGTGCAGCTGAACGAGATAGAAC 301
62 GCTAGATCGCGAAATCAG--ATGGGTGGCGGCAAGTGCAGCTGAACGAGATAGAAC 119
302 AAGATAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAAGCGCAC 361
120 AAGATAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAAGCGCAC 179
362 GAGATCTCCGCTCTGTGAGCGCGAGGTGCGCGTCACTCTTCTCCCGCAAGGCGAAC 421
180 GAGATCTCCGCTCTGTGAGCGCGAGGTGCGCGTCACTCTTCTCCCGCAAGGCGAAC 239
422 CTATAGATAGCGCCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 481
240 CTATAGATAGCGCCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 299
482 TCTTATGCTGAAGAAGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGGTCCAC 541
300 TCTTATGCTGAAGAAGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGGTCCAC 359
542 GAATACAGGAACCTTAAGCGGAGATTGAGACCATACAAAATGTCACAAGC 593
360 GAATACAGGAACCTTAAGCGGAGATTGAGACCATACAAAATGTCACAAGC 411

LOCUS B212134 694 bp mRNA linear EST 04-APR-2002
DEFINITION B212134 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
CDNA clone wh34p04 5', mRNA sequence.
B212134
B212134
B212134.1 GI:19951373
EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 694)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
Contact: Tadasi Shin-I
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES

source

Location/Qualifiers
1..694
/organism="Triticum aestivum"
/cultiivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wh34p04"
/clone_1db="Y. Ogihara unpublished cDNA library, Wh"
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid phagemids in the T7 Close Lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

BASE COUNT 211 a 181 c 189 g 113 t
ORIGIN

Query Match 66.6%; Score 394.8; DB 13; Length 694;
Best Local Similarity 99.0%; Pred. No. 1.2e-91;
Matches 408; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

182 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAAGAGCCGACA 241
2 GCGACGTCCTCCCTCTCCACCCCGCGCGCGCCATAGACACAAGAGCCGACA 61
242 GCTAGATCGCGAAATCAGATATGGTGGCGGCAAGTGCAGCTGAACGAGATAGAAC 301
62 GCTAGATCGCGAAATCAG--ATGGGTGGCGGCAAGTGCAGCTGAACGAGATAGAAC 119
302 AAGATAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAAGCGCAC 361
120 AAGATAATCGCGAGTGAACCTTCTCCAAAGCGCGCAAGGCTCTTGAAGAAGCGCAC 179
362 GAGATCTCCGCTCTGTGAGCGCGAGGTGCGCGTCACTCTTCTCCCGCAAGGCGAAC 421
180 GAGATCTCCGCTCTGTGAGCGCGAGGTGCGCGTCACTCTTCTCCCGCAAGGCGAAC 239
422 CTATAGATAGCGCCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 481
240 CTATAGATAGCGCCACCGACTCCAGATGAGCAAAATCTTGAACGTTATGAGCGCTAC 299
482 TCTTATGCTGAAGAAGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGGTCCAC 541
300 TCTTATGCTGAAGAAGCTCTTATTTCACTGAATCTGAAGTGAAGGAAATTTGGTCCAC 359
542 GAATACAGGAACCTTAAGCGGAGATTGAGACCATACAAAATGTCACAAGC 593
360 GAATACAGGAACCTTAAGCGGAGATTGAGACCATACAAAATGTCACAAGC 411

LOCUS B1956235 1196 bp mRNA linear EST 22-OCT-2001
DEFINITION B1956235 Hordeum vulgare rachis EST library, HVCN0015
(normal) Hordeum vulgare cDNA clone HVSMB0001F21f, mRNA sequence.
B1956235
B1956235
B1956235.1 GI:16306797
EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 1196)
Wang, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,

REFERENCE
AUTHORS

FRISCH, D., AKKINS, M., YU, Y., HENRY, D., PALMER, M., RAMBO, T., SIMMONS, J., OATES, R. and MAIN, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex rachis cDNA library
 Unpublished (2001)
 Contact: Ming RA
 c/o "Ming RA" Gerald@arabidopsis.org

Friedrich D., Watkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons J., Oates, R. and Main, D.,
Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library
Unpublished (2001)
Contact: Ming RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twining@clemson.edu
Total hg bases = 172
Seq primer: AATTAACCTTCACATAAGG
High quality sequence start: 3
High quality sequence stop: 1100

FEATURES	Location/Qualifiers
source	1. .1196

/organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSME0001P21f"
 /clone_lib="Hordeum vulgare rachis EST library HVCMDA0015
 (normal)"
 /tissue_type="Rachis"
 /lab_host="TJ0121"
 /note="Vector: plusscript SK(-); Site 1: EcoRI; Site 2:
 XhoI; Plants were grown at Washington State University,
 Pullman, WA in a greenhouse, the rachises were excised and
 frozen in liquid nitrogen (Kleinhof lab). In the T4 Close
 lab at the University of California, Riverside total RNA
 was prepared, poly(A) was purified, one primary
 unamplified cDNA library was made, and 1 million plv were
 in vivo excised to give plusscript SK(-) cDNA phageamids
 (Chin). Phageamids were plated and picked at the Clemson
 University Genomics Institute (CUGI) (Begum, Palmer,
 Friesch, Atkins and Wing). Plasmid DNA preparations, DNA
 sequencing and sequence analysis were performed at CUGI
 (Wing, Yu, Friesch, Henry, Simmons, Rambo, Mann). The
 sequence has been trimmed to remove vector sequence and
 contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
<http://www.genome.clemson.edu/projects/barley/>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinhof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
<http://wheat.pw.usda.gov/gpages/bgn/31/cover.html>."

BASE COUNT	278 a	439 c	270 g	172 t.	37 others
ORIGIN					

Query Match	65.1%	Score 386;	DB 13;	Length 1196;
Best Local Similarity	94.5%;	Pred. NO. 2.7e-89;		
Matches 410; Conservative	0;	Mismatches 22;	Indels 2;	Gaps 1;

OY	160	CCCTACCGCGCGGCGAGGCGCAGCAGCTGTGCGTCTCCACCCCGCGCGGTGGC	219
		1	CCCTACCGCGCGGCGGAGCACAAGAGTGTGCGTCTCCACCTCCGCGCGCGTGGC
Db			60
OY	220	GCCATAGACACAAAGCGCCGACAGTATCGCGAATCAGATATGGTTCGGCGCAAGT	279
Db	61	GCCATAGACACAGCGCCGACACTAGAGGGTGAATCGGG--ATGGGTGGCGTAAAGT	118
OY	280	GCAGTTGAACGGGATAGAAACAATATAATCGGAGGTGACCTTCTCCAAACGGCGCA	339
Db	119	GCANTGAAGCGGATAGAAACAAGTAAATGGGAGGTCGACTTCTCCAAACGGCGCA	178
OY	340	CGGCGTCTTGAAGAAGGCGCAGAGATCTCGCTCTCTTGACGCGGAGGTGGCGTCAT	399
Db	179	CGGCGTCTTGAAGAAGGCGCAGAGATCTCGCTCTCTTGACGCGGAGGTGGCGTCAT	238
OY	400	CGTCTTCTCCCCAAAGCGAGCTCTATGATGACGACCGACTCCAGCATGACAAAT	459

Db 239 CGTCTTCTCCCCAAAGCAGCTGTATGAGTAAGCCACCACTCCAGATGACAAAT 298

Qy 460 TCTTGAACGTTATGAGCGCTACTTTATGCTGAAAAAGCTCTTATTTGACTGAATCTGA 519

Db 299 TCTTGAACGTTATGAGCGCTACTTTATGCTGAAAAAGCTCTTATTTGACTGAATCTGA 358

Qy 520 AAGTAGGGAATTTGTCGCCAAGATACAGGAAACTTAAAGCGAAGATTGAGACCATACA 579

Db 359 AAGTAGGGAATTTGTCGTATCATGAATACAGGAAACTTAAAGCGAAGATTGAGACCATCA 418

Qy 580 AAAATGTCACAAGC 593

Db 419 GAAGTGGCACAAGC 432

RESULT 9	Bj213269	658 bp	mRNA	linear	EST 04-APR-2002
LOCUS	Bj213269				
DEFINITION	Bj213269	Y. Ogihara unpublished cDNA library, Wh	Triticum aestivum		
ACCESSION	Bj213269				
VERSION	Bj213269.1	GI:19952768			
KEYWORDS	EST.				
SOURCE	bread wheat.				
ORGANISM	Triticum aestivum				

REFERENCE	1 (bases 1 to 658)
AUTHORS	Ogihara, Y. and Murai, K.
TITLE	Expressed genes in <i>Triticum aestivum</i>
JOURNAL	Unpublished (2002)
COMMENT	Contact: Tadasu Shin-i

Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsuhini@genes.nig.ac.jp.

FEATURES	location/Qualifiers
source	1. .658

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/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="wn2132"
/clone_id="Y. Ogihara unpublished cDNA library, Wn"
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid:
Site_1: EcoRI, Site_2: XhoI. Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give plasmid preparations in the Tj Close lab
at the University of California, Riverside (Akhunov, Chinn,
Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

```

Query Match	55.0%	Score 385.4	DB 13	Length 658
Best Local Similarity	99.0%	Pred. No. 3.2e-89		
Matches 409	Conservative	0	Mismatches 1	Indels 3
			Gaps 2	
QY	182	GGAGAGTCTCGCCCTCTCTCCACCCCGCGCGCGCGCGGCATAG-ACACAAGAGCCAC	240	
Db	6	GGAGAGTCTCGCCCTCTCTCCACCCCGCGCGCGCGGCATAGTACAACAAGGCCAC	65	

OY 241 AGCTGATCGGAATTCGATATGGTCCGCGCAGGTGCACTGAAAGCGGATGAGAA 300
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 DB 66 AGTAGATCGGGAATCAGG--ATGGTTCGCGGCAAGGTGCGAGTGAAGCGGATGAGAA 123
 OY 301 CAAGTAATCGGCGGAGTACCTTCTCAAGCGCGGCAAGCGGCTCCGAAAGAGCGCA 360
 |||||
 DB 124 CAAGTAATCGGCGGAGTACCTTCTCAAGCGCGGCAAGCGGCTCCGAAAGAGCGCA 183
 OY 361 CGAGATCTCCGTCCTCTGTGACGCGGAGAGTCCGCTCAATCTCTTCCCAAGGCA 420
 184 CGAGATCTCCGTCCTCTGTGACGCGGAGAGTCCGCTCAATCTCTTCCCAAGGCA 243
 OY 421 GCTCTATGATACCGCCAGCTCCAGCATGAGCAAAATCTTGAACCTTATGACGCTA 480
 DB 244 GCTCTATGATACCGCCAGCTCCAGCATGAGCAAAATCTTGAACCTTATGACGCTA 303
 OY 481 CTCTATGCTGAAAGGCTTATTTGACCTGAACTGAAAGTGGGAAATTTGTTGCA 540
 DB 304 CTCTATGCTGAAAGGCTTATTTGACCTGAACTGAAAGTGGGAAATTTGTTGCA 363
 DB 541 CGAATACGAGAACTTAAGCGGAGATTGAGACCATACAAATGTCCACAAGC 593
 364 CGAATACGAGAACTTAAGCGGAGATTGAGACCATACAAATGTCCACAAGC 416

RESULT 10
 BE498620 551 bp mRNA linear EST 04-AUG-2000
 LOCUS dectivum_cDNA clone WHE0964_G04_M08, mRNA sequence.
 DEFINITION WHE0964_G04_M0825 wheat pre-anthesis spike cDNA library Triticum
 BE498620
 VERSION BE498620.1 GI:9697237
 KEYWORDS EST.

SOURCE

ORGANISM
 Triticum aestivum

REFERENCE
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Heia, C.C., Kang, Y., Iazo, G.R., Miller, R., Rauech, C.J., Seaton, C.J., and Tong, J.C.
 The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
 Unpublished (2000)

JOURNAL

COMMENT
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

FEATURES

source

1..551
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0964_G04_M08"
 /clone_lib="wheat pre-anthesis spike cDNA library"
 /tissue_type="Spike before anthesis"
 /dev_stage="Adult plant"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site 1: EcoRI, Site 2: XhoI; plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA

BASE COUNT 162 a 141 c 143 g 105 t
 ORIGIN
 preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

Query Match 64.8%; Score 384.4; DB 10; Length 551;
 Best Local Similarity 99.2%; Pred. No. 5.5e-89;
 Matches 397; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

OY 194 CTCCTCCACCCCGCGCGCGGCGGCGCATAGACAGAGCGGACGCTAGATCGGA 253
 DB 1 CTCCTCCACCCCGCGCGCGGCGGCGCATAGACAGAGCGGACGCTAGATCGGA 60
 OY 254 AATCAGATATAGGTCGCGGCAAGTCCAGTGAAGCGGATAGAAACAATATTCG 313
 DB 61 AATCAGG--ATGGTCCCGGAGAGTCACTGAGCGGATAGAAACAATATTCG 118
 OY 314 CAGGTGACCTTCTTCCAAAGCGCGGCAAGGCTCTTGAAGAGGCGCACAGATCTCGTC 373
 DB 119 CAGGTGACCTTCTTCCAAAGCGCGGCAAGGCTCTTGAAGAGGCGCACAGATCTCGTC 178
 OY 374 CTCTGTACGCGGAGGTGCGCGTCAATGCTTCTCCCAAGGCAAGCTTATGATAC 433
 DB 179 CTCTGTACGCGGAGGTGCGCGTCAATGCTTCTCCCAAGGCAAGCTTATGATAC 238
 OY 434 GCCACGACTTCACATGACGCAAAATCTTGAACGTTATGAGCCTACTTATGCTGAA 493
 DB 239 GCCACGACTTCACATGACGCAAAATCTTGAACGTTATGAGCCTACTTATGCTGAA 298
 OY 494 AAGGCTCTTATTTGAGTGAATCTGAAAGTGAAGAAATTTGTCGCAAGTACAGAAA 553
 DB 299 AAGGCTCTTATTTGAGTGAATCTGAAAGTGAAGAAATTTGTCGCAAGTACAGAAA 358
 OY 554 CTTAAGCGGAAAGTGAACCATACAAATGTCCACAAGC 593
 DB 359 CTTAAGCGGAAAGTGAACCATACAAATGTCCACAAGC 398

RESULT 11

LOCUS B1957545 622 bp mRNA linear EST 22-OCT-2001
 DEFINITION HVSMEN0010B09f Hordeum vulgare rachis EST library HVCNDN0015
 (normal) Hordeum vulgare cDNA clone HVSMEN0010B09f, mRNA sequence.

JOURNAL

COMMENT
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu

FEATURES

source

1..622
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 TITLE
 Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
 Unpublished (2001)
 JOURNAL
 COMMENT
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Total hg bases = 419
 Seq primer: AATTACCTCCTCACTAAAGG
 High quality sequence stop: 591.
 Location/Qualifiers

Accession BOJ78659 mRNA sequence.
Version BOJ78659.1 GI:21987131
Keywords EST.
Source Zea mays.
Organism Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
Reference 1 (bases 1 to 572)
Authors Walbot V.
Title Maize ESTs from various cDNA libraries sequenced at Stanford University
Journal Unpublished (1999)
Comment Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 94613 row: A column: 11.
Location/Qualifiers
1..572
/organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tassels primordium prepared by Schmidt lab"
/tissue_type="tassels"
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/lab_host="X10LR"
/note="Organ: tassels; Vector: HybriZAP; Site_1: EcorI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 Kb with a 1 Kb average."
148 a 179 c 147 g 98 t
BASE COUNT
ORIGIN
Query Match 51.3%; Score 304; DB 14; Length 572;
Best Local Similarity 79.2%; Pred. No. 3.6e-68;
Matches 374; Conservative 0; Mismatches 95; Indels 3; Gaps 1;
122 CCTTCTCTCCCATCTTAAGTGCATCCATCTCCCTCACCGCGCGGAGCA 181
50 CCTCCCGATCCCTCTTCACTCACTCTTTAAAGCTACCGACTACCTGCT 109
182 GCGACGTCGCTCTCTCCACCCGCGCGCGCGCATAGACACAGAGCGACA 241
110 GCGTCGCTCAACTCGCGCGCGCGCGCATAGACCGGAGAGAGAGAGCA 169
242 GCTAGATCGCAATCAGATATGGGTGGCGCAAGTGCAGCTGAACGGATAGAC 301
170 GATG---GAGGCGAGCGAAGATGGGCGCGCAAGGTGAGTGAACGATAGAAC 226
302 AAGATTAATGGGCGAGTGAACCTTCTCCAGCGCGCAACGGGCTCTTAAGAAGCGGAC 361
227 AAGATTAACCGGCGAGCGAATCTTCCAGGCGCGAAGCGGCTGTGAAGAGCGGAC 286
362 GAGATCTCGCTCTGTGAGCGGAGGTGCGCGCATCTCTCTCCCGAAGGCGAG 421
287 GAGATCTCGCTCTGTGAGCGGAGGTGCGCGCATCTCTCTCCCGAAGGCGAG 346
422 CTATATGAGTACGCCACCGACTCCAGATGACAAATTTCTGAACGTTATGAGCGCTAC 481
347 CTATACGAGTACGCTCCGATCCCGCATGACAAATTTCTGAACGTTATGAGGATAT 406
482 TCTATATGCTGAAGGCTCTTATTCAGCTGAATCTGAATGAGGAGAAATTTGGTCCAC 541
407 TCTATATGCTGAAGGCTCTTATTCAGCTGAATCTGAATGAGGAGAAATTTGGTCCAC 466

RESULT 14
LOCUS AY109845. 1488 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays CL2300_1 mRNA sequence.
ACCESSION AY109845
VERSION AY109845.1 GI:21213723
KEYWORDS HTC.
SOURCE Zea mays.
Organism Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
Reference 1 (bases 1 to 1488)
Authors Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Title Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
Journal Unpublished (2002)
Reference 2 (bases 1 to 1488)
Authors Coe, E.C.
Title Direct Submission
Journal Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
Location/Qualifiers
1..1488
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/db_xref="taxon:4577"
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
BASE COUNT 285 a 288 c 292 g 238 t 385 others
ORIGIN
Query Match 49.0%; Score 290.4; DB 11; Length 1488;
Best Local Similarity 89.5%; Pred. No. 1.6e-64;
Matches 306; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
252 GAATACGAGATATGCTGCGGCAAGGTGACGATGAGACGATTAATC 311
138 GCAACAAAGCGATGGGCGCGCAAGGTACGCTGAAGCGATGAACAAGATTAAC 197
312 GCGAGTACCTTCTCCAGGCGCGCAAGGCTCTGAAGAGAGCGCAGATCTCG 371
198 GCGAGTACCTTCTCCAGGCGCGCAAGGCTCTGAAGAGAGCGCAGATCTCG 257
372 TCTCTGTGACGCGGAGGTGCGCTCATCTCTTCTCCCGAAGGCAAGCTTATGAGT 431
258 TCTCTGTGACGCGGAGGTGCGCTCATCTCTTCTNNNNNAAGGCAAGCTTACGAGT 317
432 ACGGCAACGCTCCGAGATGAGCAAAATTTCTGAACGTTATGAGCGCTACCTTATGCTG 491
318 ACGGCAACGCTCCGAGATGAGCAAAATTTCTGAACGTTATGAGCGCTATGCTG 377
492 AAAAGCTCTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGGTGCAGAAATACAGA 551
378 AAAAGCTCTTATTTACGCTGAATCTGAAGTGAAGGAAATTTGGTGCAGAAATACAGA 437
552 AACTTAAGGCGAAGATTGAGACCATTAACAAATTTGTCAAGC 593
438 AACTGAAGGCGCAAAATTTGAAGCATACNNNNNTGCCAAGC 479

01-OCT-2000 (TREMBlrel. 15, Last sequence update)
01-MAR-2002 (TREMBlrel. 20, Last annotation update)
MADS-box protein 5.
M5.
Hordium vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
NCBI_TaxID=4513;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ATLAS; TISSUE=FLOWER;
RX MEDLINE=20346590; PubMed=10890536;
RA Schmitz J., Franzen R., Nguyen T., Garcia-Maroto F., Pozzi C.,
RA Salami F., Rohde W.,
RT "Cloning, mapping and expression analysis of six barley MADS-box
genes";
RL Plant Mol. Biol. 42:899-913(2000).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
EMBL; AJ249144; CAB57352.1; -.
DR HSSP; P11746; 1NMN.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
KW SEQUENCE 244 AA; 28093 MW; 4732EBBD28153879 CRC64;

Alignment Scores:
Pred. No.: 1.95e-35 Length: 244
Score: 484.00 Matches: 92
Percent Similarity: 92.73% Conservative: 10
Best Local Similarity: 83.64% Mismatches: 8
Query Match: 46.99% Indels: 0
DB: 10 Gaps: 0

US-10-020-338-8 (1-593) x Q9LE12 (1-244)

0Y 263 ATGGTCCGCGCAAGTGCAGTGAAGCGGATAGAGCAAGATTAATCCGAGTGAAC 322
DB 1 MetGlyArgArgValGlnLeuLysArgIleGlnLysLeuLysValLeuValThr 20
0Y 323 TTCTCCAGAGCGCGCAAGCGGCTCTGAAGAAGCGGACGAGATCTCGCTCTGTGAC 382
DB 21 PheSerLysArgArgGlyLeuLeuLysLysAlaHisGlnIleSerValLeuThrAsp 40
0Y 383 GCGAGGTGCGCGTATGCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValIleValPheSerHisLysGlyLeuValGluPheSerThrGlu 60
0Y 443 TCCGACGACGCAAAATTTCTGAAGCTTATGAGCGCTCTTATGCTGAAGGCTTT 502
DB 61 SerCysMetAspLysIleLeuGlnArgGlyGlnValGlySerValGlnValLeu 80
0Y 503 ATTTCAGTGAATCTGAAGAAGTGAAGAAATTTGTCGCCAGATACAGAAATTAAAGCG 562
DB 81 ValIleSerGlnSerGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 100
0Y 563 AAGATTGAGACCATACAAAATGTCACAG 592
DB 101 LysValGlnThrIleGlnLysCysGlnLys 110

RESULT 15

039399 PRELIMINARY; PRT; 243 AA.
AC 039399;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

01-MAR-2002 (TREMBlrel. 20, Last annotation update)
MADS3 protein.
MADS3.
Betula verrucosa (White birch) (Betula pendula).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eustoidia I; Fagales; Betulaceae; Betula.
NCBI_TaxID=3505;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=FEMALE INFLORESCENCE;
RA Elo A., Lemmetyinen J., Turunen M.L., Tikka L., Sopanen T.;
RT "Three MADS box genes homologous to SOUMOSA and APETALA1 have
different expression patterns in silver birch (Betula pendula
Roth.)";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
EMBL; X99653; CA67967.1; -.
DR HSSP; P11746; 1NMN.
DR TRANSFAC; T03046; -.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
KW SEQUENCE 243 AA; 27925 MW; 2E5861F1A09D04F CRC64;

Alignment Scores:
Pred. No.: 5.39e-32 Length: 243
Score: 446.00 Matches: 85
Percent Similarity: 90.00% Conservative: 14
Best Local Similarity: 77.27% Mismatches: 11
Query Match: 43.30% Indels: 0
DB: 10 Gaps: 0

US-10-020-338-8 (1-593) x Q39399 (1-243)

0Y 263 ATGGTCCGCGCAAGTGCAGTGAAGCGGATAGAGCAAGATTAATCCGAGTGAAC 322
DB 1 MetGlyArgArgValGlnLeuLysArgIleGlnLysLeuLysValLeuValThr 20
0Y 323 TTCTCCAGAGCGCGCAAGCGGCTCTGAAGAAGCGGACGAGATCTCGCTCTGTGAC 382
DB 21 PheSerLysArgArgGlyLeuLeuLysLysAlaHisGlnIleSerValLeuThrAsp 40
0Y 383 GCGAGGTGCGCGTATGCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValIleValPheSerHisLysGlyLeuValGluPheSerThrGlu 60
0Y 443 TCCGACGACGCAAAATTTCTGAAGCTTATGAGCGCTCTTATGCTGAAGGCTTT 502
DB 61 SerCysMetGlnLysIleLeuGlnArgGlyGlnValGlySerValGlnValLeu 80
0Y 503 ATTTCAGTGAATCTGAAGAAGTGAAGAAATTTGTCGCCAGATACAGAAATTAAAGCG 562
DB 81 ValIleSerGlnSerGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 100
0Y 563 AAGATTGAGACCATACAAAATGTCACAG 592
DB 101 LysValGlnThrIleGlnLysCysGlnLys 110

Search completed: June 24, 2003, 14:12:17
Job time : 52 secs

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DT 01-OCT-2000 (TREMBLrel. 15, Created)

OY 563 AAGATTGAGACCATACAAAATGTCACAG 592
Db 101 LysValGluThrIleGlnLysCysGlnLys 110

RESULT 10

O9ZTT7 PRELIMINARY; PRT; 245 AA.

AC O9ZTT7
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MADS-box protein 1.
GN MADS1.
OS Lolium temulentum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Lolium.
NCBI_TaxID=34176;
[1]
SEQUENCE FROM N.A.
RC STAIN=CERES;
RA Gocal G.F.W., Blundell C., Schwartz O.M., King R.W.;
RT "Expression of Two APERLAI-Related Genes Changes During Inflorescence
Initiation of Lolium."
RL Submitted (NOV-1997) to the EMBL/GenBank/DBSJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF035378; AAD10625.1; -
DR HSSP; P11831; 1SRS.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 245 AA; 28039 MW; 5C4BEF15903ACC39 CRC64;

Alignment Scores:

Pred. No.: 1.62e-37 Length: 245
Score: 507.00 Matches: 96
Percent Similarity: 93.64% Conservative: 7
Best Local Similarity: 87.27% Mismatches: 7
Query Match: 49.22% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x O9ZTT7 (1-245)

OY 263 ATGGGTGCGGCGCAAGTGCAGCTGAAGCGGATAGAAACAGATTAATCGGAGGTGACC 322
Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLeuLysIleAsnArgGlnValThr 20
OY 323 TTCTCCAGCGCGCGCAAGCGGCTCTGAAGAGCGGCGAGATCTCGTCTCTGTGAC 382
Db 21 PheSerLysArgArgSerLysLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
OY 383 GCGAGGTGCGCGCATGCTCTTCTCCCGCAAGGCAAGCTCTATGATGACCGACCGAC 442
Db 41 AlaGlnValAlaLeuIleIlePheSerThrLysGlyLysLeuLysGlnPheIleThrAsp 60
OY 443 TCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTTATGCTGAAGAGCTCTT 502
Db 61 SerCysMetAspLysIleLeuGlnArgLysGlyArgLysSerValAlaGlnLysValLeu 80
OY 503 ATTTCAGTGAATCTGAAGAGTGAAGAAATTTGTCGCGCATGACGAAATCTTAAGCGG 562
Db 81 IleSerThrGlnSerGlnLysGlnGlnLysAsnTrpCysHisGlnLysValLysValAla 100
OY 563 AAGATTGAGACCATACAAAATGTCACAG 592
Db 101 LysValGluThrIleGlnLysCysGlnLys 110

Db 101 LysValGluThrIleGlnArgCysGlnLys 110

RESULT 11

O9SEXO PRELIMINARY; PRT; 246 AA.

AC O9SEXO
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE MADS14 protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubartoidae; Oryzaeae; Oryza.
NCBI_TaxID=4530;
[1]
SEQUENCE FROM N.A.
RC TISSUE=FLOWER;
RA MEDLINE=99373407; Pubmed=10444103;
RA Moon Y.H., Kang H.G., Jung J.Y., Jeon J.S., Sung S.K., An G.;
RT "Determination of the motif responsible for interaction between the
rice APERLAI/AGAMOUS-LIKE9 family proteins using a yeast two-hybrid
system."
RL Plant Physiol. 120:1193-1204(1999).
DR EMBL; AF058697; AAF19047.1; -
DR HSSP; P11831; 1SRS.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; UNKNOWN_1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
SQ SEQUENCE 246 AA; 28523 MW; 3044628F2840AC53 CRC64;

Alignment Scores:

Pred. No.: 1.62e-37 Length: 246
Score: 507.00 Matches: 97
Percent Similarity: 95.45% Conservative: 8
Best Local Similarity: 88.18% Mismatches: 5
Query Match: 49.22% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x O9SEXO (1-246)

OY 263 ATGGGTGCGGCGCAAGTGCAGCTGAAGCGGATAGAAACAGATTAATCGGAGGTGACC 322
Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLeuLysIleAsnArgGlnValThr 20
OY 323 TTCTCCAGCGCGCGCAAGCGGCTCTGAAGAGCGGCGAGATCTCGTCTCTGTGAC 382
Db 21 PheSerLysArgArgSerLysLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
OY 383 GCGAGGTGCGCGCATGCTCTTCTCCCGCAAGGCAAGCTCTATGATGACCGACCGAC 442
Db 41 AlaGlnValAlaLeuIleIlePheSerThrLysGlyLysLeuLysGlnPheIleThrAsp 60
OY 443 TCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTTTATGCTGAAGAGCTCTT 502
Db 61 SerCysMetAspLysIleLeuGlnArgLysGlyArgLysSerValAlaGlnLysValLeu 80
OY 503 ATTTCAGTGAATCTGAAGAGTGAAGAAATTTGTCGCGCATGACGAAATCTTAAGCGG 562
Db 81 IleSerThrGlnSerGlnLysGlnGlnLysAsnTrpCysHisGlnLysValLysValAla 100
OY 563 AAGATTGAGACCATACAAAATGTCACAG 592
Db 101 LysValGluThrIleGlnLysCysGlnLys 110
RESULT 12
O9M7C6 PRELIMINARY; PRT; 246 AA.

Db 41 AlaciuValAlaAlaIleValPheSerProlysglyLysleuTyrGluTyrAlaThrAsp 60
QY 443 TCACGATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAGAGCTCTT 502
Db 61 SerArgMetAspLysIleleuGluLysTyrGluLysTyrSerTyrAlaGluLysAlaIleu 80
QY 503 ATTTGAGCTGAATCTGAAGAGGAAATGCTGCTCCAGCAATACAGGAATCTTAAGCG 562
Db 81 IleSerAlaGluSerGluSerGluLysGluLysAsnTyrCysHisGluTyrArgLysleuLysAla 100
QY 563 AAGATTGAGACCATCAAAATGTCAAG 592
Db 101 LysIleGluThrIleGlnIleCysHisLys 110
RESULT 8
ID 004068 PRELIMINARY; PRT: 228 AA.
AC 004068:
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
MADS box protein (Fragment).
OS Sorghum bicolor (Sorghum) (Sorghum vulgare).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Sorghum.
OX NCBI_TaxID=4558;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97218034; PubMed=9065695;
RA Greco R., Stegi L., Colombo L., Angenent G.C., Sari-Gorla M., Pe M.E.,
RT "MADS box genes expressed in developing inflorescences of rice and
RT sorghum."
RL Mol. Gen. Genet. 253:615-623 (1997).
DR EMBL: U32110; AAB50181.1; -.
DR HSSP: P11831; ISRS.
DR TRANSFAC: T03172; -.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR NON TER 1
FT SEQUENCE 228 AA; 25999 MW; 3F70A30B6E23CC25 CRC64;
SQ
Alignment Scores:
Pred. No.: 2.03e-40 Length: 228
Score: 539.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 52.33% Indels: 0
Gaps: 0
US-10-020-338-8 (1-593) x 004068 (1-228)
QY 275 AAGGTGCGTGAAGCGGATAGAGAAAGATTAATCGGAGTGAAGCTTCTTCAAGCC 334
Db 1 LysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThrPheSerLysArg 20
QY 335 CGCAAGCGGCTCCCTGAAGAGCGCAGAGATCTCGCTCTGTGAGCGGAGGCTGCC 394
Db 21 ArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuCysAspAlaGluValAla 40
QY 395 GTCAATGCTTCTCCCAAGGCAAGCTCTATGAGTACGCCAGCATCCAGCATGAGC 454
Db 41 ValIleValPheSerProlysglyLysleuTyrGluTyrAlaThrAspSerArgMetAsp 60
QY 455 AAAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAGAGCTCTTATTTCACTGAA 514
Db 61 LysIleleuGluLysTyrGluLysTyrSerTyrAlaGluLysAlaIleuIleSerAlaGlu 80

QY 515 TCTGAAGTGAAGGAAATTTGCTGCCACGAATACGAAATCTTAAGCGGAGATTGAGACC 574
Db 81 SerGluSerGluGlyAsnTyrCysHisGluTyrArgLysleuLysAlaLysIleGluThr 100
QY 575 ATACAAATGTCAACAG 592
Db 101 IleGlnLysCysHisLys 106
RESULT 9
ID 09MAY7 PRELIMINARY; PRT: 246 AA.
AC 09MAY7:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE AP1-like MADS box protein.
GN RAP1B.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Kyzuka J., Kobayashi T., Morita M., Shimamoto K.,
RT "Spatially and temporally regulated expression of rice MADS box genes
RT with similarity to Arabidopsis class A, B, C genes."
RL Plant Cell Physiol. 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AB041020; BAA94342.1; -.
DR HSSP: P11831; ISRS.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 246 AA; 28489 MW; DF357FC94FB5B2FD CRC64;
Alignment Scores:
Pred. No.: 3.05e-38 Length: 246
Score: 515.00 Matches: 98
Percent Similarity: 96.36% Conservative: 8
Best Local Similarity: 89.09% Mismatches: 4
Query Match: 50.00% Indels: 0
Gaps: 0
US-10-020-338-8 (1-593) x 09MAY7 (1-246)
QY 263 ATGGGTGCGCGCAAGGTGACGCTGAAGCGGATAGAGAAAGATTAATCGGAGTGAAC 322
Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTTCAAGCGCCCAAGCGGCTCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuCysAsp 40
QY 383 GCGAGGCGCGCATGCTTCTTCCCAAGGCAAGCTCTATGAGTACGCCAGCGAC 442
Db 41 AlaciuValAlaLeuIleIlePheSerThrLysGlyLysleuTyrGluTyrAlaThrAsp 60
QY 443 TCACGATGACAAATTTCTTGAACGTTATGAGCGCTACTTATGCTGAAGAGCTCTT 502
Db 61 SerGlyMetAspLysIleleuGluLysTyrGluLysTyrSerTyrAlaGluLysValleu 80
QY 503 ATTTGAGCTGAATCTGAAGAGGAAATTTGCTGCTCCAGCAATACAGGAATCTTAAGCGCG 562
Db 81 IleSerAlaGluSerAspThrGlnGlnLysAsnTyrCysHisGluTyrArgLysleuLysAla 100

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DB: 10 Gaps: 0
US-10-020-338-8 (1-593) x Q9SEW9 (1-267)
OY 263 ATGGGTCCGCGCAAGCTGCAGTGAAGCGGATAGACAAACAGATAATCGGAGCTGACC 322
Db 1 MetGlytArgGlyLlyValGlnleuSuYsArgIleGluAsnIleleuAenArgInValThr 20
OY 323 TTCTCCAGACCGCGCAACCGGCTCCCGAAGAAGCGGCACAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgArgAsnGlyLeuLeuSuLYsAlaHisGlnIleleuValLeuCySAsp 40
OY 383 GCGAGAGTCGCGCGTATCTGCTCTTCCGCCCAAGGCAAGCTCATATAGTACGCCACGAC 442
Db 41 AlaGluValAlaAlaIleValPheSerProLYsGlyLlyLeuLeuYrGluYrAlaThrAsp 60
OY 443 TCCAGCAATGACCAAAATTTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAAGCTCTT 502
Db 61 SerArgMetAspLysIleleuGlnArgYrGlyArgYrSerYrAlaGluLYsAlaLeu 80
OY 503 ATTCAGCTGATCTCGAAGTGAAGTGAAGGAAATTTGGTGCACGAAATACGAAACTTAAGGCG 562
Db 81 IleSerAlaIleuSerGlnuSerGluuGlyAsnTrpCyHisGluYrArgLYsLeuLYsAla 100
OY 563 AAGATTGAGACCATACCAAAATGTCAAG 592
Db 101 LysIleGluThrIleGlnIlyScyHisLYs 110
RESULT 6
OYFR84 PRELIMINARY; PRT; 270 AA.
AC OYFR84;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MADS box protein 3.
GN MADS3.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
CN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=A186;
RC MEDLINE=21437929; PubMed=11553732;
RA Heuer S., Hansen S., Bantlin J., Bretschneider R., Kranz E., Lorz H.,
Dresselhaus T.;
"the maize MADS box gene ZmMADS3 affects node number and spikelet
development and is co-expressed with ZmMADS1 during flower
development, in egg cells, and early embryogenesis.";
RL Plant Physiol. 127:33-45(2001).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL; AF131150; AAC43200.1; -
DR HSSP; P11831; 1SR8.
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRF-TF; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
KW SEQUENCE 270 AA; 3103 MW; 253CA21C3ED5B5FD CRC4;

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Alignment Scores:	
Pred. No.:	9.09e-42
Score:	554.00
Percent Similarity:	99.09%
Best Local Similarity:	97.27%
Query Match:	53.79%
Length:	270
Matches:	107
Conservative:	2
Mismatches:	1
Indels:	0

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DB: 10 Gaps: 0
US-10-020-338-8 (1-593) x Q9FR84 (1-270)
QY 263 ATGGGTCGGCGCAAGGTGACGCTGAAGCGGATAGAGAAACAAGATTAATCGCAGGTGACC 322
Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLeuLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCCGCAAGGGGCTCTCTGAAGAAAGCGCGCACGAGATCTCCGCTCTTGAC 382
Db 21 PheSerLysArgArgSnmIleuLeuLysLysAlaHisGluIleSerValLeuCyasp 40
QY 383 GCGGAGGTGCGCGTCACTGCTCTTCCCGCCAAAGCGCAAGCTCTATGAGTACGCCACGAC 442
Db 41 AlGlnValAlaValIleValPheSerProLysGlyLysLeuTyrGlnTyrAlaSerAsp 60
QY 443 TCAGAGATGAGCAAAATTTCTGAAGCTTATGACGCGCTACTCTTATGCTGAAGAGCTTT 502
Db 61 SerArgMetAspLysIleLeuGlnLysArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
QY 503 ATTTACGCTGATCTTGAAAGATGAGGAAATTGTCGCCGAAATACAGGAACTTAAGCGC 562
Db 81 IleSerAlaGlnSerLysLeuLysLeuLysAntpCysHisGlnTyrArgLysLysAla 1000
QY 563 AAGATTGAGCCATACAAAATATGTCACAG 592
Db 101 LysIleGlnLysIleGlnLysArgCysHisLys 110

RESULT 7
Q947B8 PRELIMINARY; PRT; 267 AA.
ID Q947B8
AC Q947B8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MADS-box protein FDRMADS3.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaeae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao Z., Chen R., Jia H., Sun C.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF345911; AL009473.1; -.
DR InterPro: IPR002487; TrEMBL.
DR InterPro: IPR002100; TrEMBL.
DR Pfam; PF01486; K-box; 1.
DR Pfam; PF00319; SRP-Tr; 1.
DR PROSITE; PSS0066; MADS_BOX_2; 1.
SQ SEQUENCE 267 AA; 31266 MW; 1003B3419DED35CD CRC64;

Alignment Scores:
Pred. No.: 2,576-41 Length: 267
Score: 549.00 Matches: 106
Percent Similarity: 97.27% Conservative: 1
Best Local Similarity: 96.36% Mismatches: 3
Query Match: 53.30% Indels: 0
DB: 10 Gaps: 0

US-10-020-338-8 (1-593) x Q947B8 (1-267)
QY 263 ATGGGTCGGCGCAAGGTGACGCTGAAGCGGATAGAGAAACAAGATTAATCGCAGGTGACC 322
Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLeuLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCCGCAAGGGGCTCTCTGAAGAAAGCGCGCACGAGATCTCCGCTCTTGAC 382
Db 21 PheSerLysArgArgSnmIleuLeuLysLysAlaHisGluIleSerValLeuCyasp 40
QY 383 GCGGAGGTGCGCGTCACTGCTCTTCCCGCCAAAGCGCAAGCTCTATGAGTACGCCACGAC 442
Db 41 AlGlnValAlaValIleValPheSerProLysGlyLysLeuTyrGlnTyrAlaSerAsp 60
QY 443 TCAGAGATGAGCAAAATTTCTGAAGCTTATGACGCGCTACTCTTATGCTGAAGAGCTTT 502
Db 61 SerArgMetAspLysIleLeuGlnLysArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
QY 503 ATTTACGCTGATCTTGAAAGATGAGGAAATTGTCGCCGAAATACAGGAACTTAAGCGC 562
Db 81 IleSerAlaGlnSerLysLeuLysLeuLysAntpCysHisGlnTyrArgLysLysAla 1000
QY 563 AAGATTGAGCCATACAAAATATGTCACAG 592
Db 101 LysIleGlnLysIleGlnLysArgCysHisLys 110

383 GCGGAGGTGCGCGTCACTGCTCTTCCCGCCAAAGCGCAAGCTCTATGAGTACGCCACGAC 442
443 GCGGAGGTGCGCGTCACTGCTCTTCCCGCCAAAGCGCAAGCTCTATGAGTACGCCACGAC 442

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Pred. No.:	2, 57e-41	Length:	267
Score:	549.00	Matches:	106
Percent Similarity:	97.27%	Conservative:	1
Best Local Similarity:	96.36%	Mismatches:	3
Query Match:	53.30%	Indels:	0
DB:	10	Gaps:	0
US-10-020-338-8 (1-593) x Q947B8 (1-267)			
QY	263	ATGGTGTGGCGGCAAGGTGCAGCTGAAGCGCGATAGAGAACCAAGATTAATTCGCGAGGTGACC	322
Db	1	MeEGLYARGGLylySValJInleuuySaGllIEGuAnSerMetAsnArgGlnValThr	20
QY	323	TTCTTCGAAGCGCGCAACGGGCTCCGTAAGAAGCGCAGAGATTCCTCGCTCTGTGAC	383
Db	21	PheserIyArgrIgrAnsnGlyleuIeuuySlySalAhISGllIESeVallleuCyasp	40
QY	383	GCGGAGGTGGCGGTCAATCGTCTTTCTCCCAAGGCAAGCTCTATGAGTACGCCACGAC	442

DR EMBL: AJ249146; CAB97354.1; -
DR HSSP: P11831; 1SRS.
DR TRANSFAC: T04768; -
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR PRINTS: PR01574; TUBERYPROTEIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 276 AA; 31839 MW; D6B9D1DC5E30B3B3 CRC64;

Alignment Scores:

Pred. No.:	7.47e-43	Length:	276
Score:	566.00	Matches:	110
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	54.95%	Indels:	0
DB:	10	Gaps:	0

US-10-020-338-8 (1-593) x Q9LE10 (1-276)

OY 263 ATGGGTGGCGGCAAGTGTGACGCTGACGAGGATAGAGAACAGATTAATCCGACAGTGACC 322
DB 1 MetGlyarGgLySVaIGlnLeuLySaRgIlleGlnuLnLySlEaSnArGdInValThr 20
OY 323 TTCTTCAAGCGCGGCAAGCGGCTCTTGAAGAGCGACGAGATCTCGTCTGTGAC 382
DB 21 PheSerLySaRgArGaSnGlyLeuLeuLySaLaHISGlnLeuSerValLeuCyAsp 40
OY 383 GCGGAGTGGCGGCTGATGCTTCTTCCGCCAAAGCAAGCTTATGAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValAlValPheSerProLySgLySLeUyRgLyTyrAlaGlnLySaLa 60
OY 443 TCCAGCATGACCAAAATCTTGAAGCTTATGAGGCTCTTATGCTGAAAAGGCTCTT 502
DB 61 SerSerMetAspLySlLeuGlnArGlyRgLnArGlyrSerTyRAlaGlnLySaLaLeu 80
OY 503 ATTTCAGTGAATGTGAAGTGAAGGAATTGGTCCACGATACAGAACTTAAGCG 562
DB 81 IleSerAlaGlnSerGlnSerGlnGlnLyAsnTrpCyShISgLnTyRArgLySLeUySaLa 100
OY 563 AAGATTGAGACCATACAAAATGTCAACAG 592
DB 101 LysIleGlnThrIleGlnLyCyShISlys 110

RESULT 2

ID	Q9ZTT6	PRELIMINARY;	PRT;	261 AA.
AC	Q9ZTT6;			
DT	01-MAY-1999 (TREMBLrel. 10, Created)			
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	MADS-box protein. 2.			
GN	MADS2.			
OS	Lolium temulentum.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;			
OC	Poaceae; Lolium.			
OC	NCBI_TaxID=34176;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CERES;			
RA	Gocal G.F.W., Blundell C., Schwartz O.M., King R.W.;			
RT	"Expression of Two APETAL-Related genes Changes During Inflorescence			
RT	Initiation of Lolium."			
RT	Submitted (Nov-1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.			
DR	EMBL; AF035379; AAD10626.1; -			

DR HSSP: P11831; 1SRS.
DR InterPro: IPR002487; TF_Kbox.
DR InterPro: IPR002100; TF_MADSbox.
DR Pfam: PF01486; K-box; 1.
DR Pfam: PF00319; SRF-TF; 1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 2.
DR DNA-binding; Nuclear protein; Transcription regulation.
SQ SEQUENCE 261 AA; 30025 MW; 176358FE0D8AAC09 CRC64;

Alignment Scores:

Pred. No.:	9.13e-43	Length:	261
Score:	565.00	Matches:	109
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	99.09%	Mismatches:	0
Query Match:	54.85%	Indels:	0
DB:	10	Gaps:	0

US-10-020-338-8 (1-593) x Q9ZTT6 (1-261)

OY 263 ATGGGTGGCGGCAAGTGTGACGCTGACGAGGATAGAGAACAGATTAATCCGACAGTGACC 322
DB 1 MetGlyarGgLySVaIGlnLeuLySaRgIlleGlnuLnLySlEaSnArGdInValThr 20
OY 323 TTCTTCAAGCGCGGCAAGCGGCTCTTGAAGAGCGACGAGATCTCGTCTGTGAC 382
DB 21 PheSerLySaRgArGaSnGlyLeuLeuLySaLaHISGlnLeuSerValLeuCyAsp 40
OY 383 GCGGAGTGGCGGCTGATGCTTCTTCCGCCAAAGCAAGCTTATGAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValAlValPheSerProLySgLySLeUyRgLyTyrAlaGlnLySaLa 60
OY 443 TCCAGCATGACCAAAATCTTGAAGCTTATGAGGCTCTTATGCTGAAAAGGCTCTT 502
DB 61 SerSerMetAspLySlLeuGlnArGlyRgLnArGlyrSerTyRAlaGlnLySaLaLeu 80
OY 503 ATTTCAGTGAATGTGAAGTGAAGGAATTGGTCCACGATACAGAACTTAAGCG 562
DB 81 IleSerAlaGlnSerGlnSerGlnGlnLyAsnTrpCyShISgLnTyRArgLySLeUySaLa 100
OY 563 AAGATTGAGACCATACAAAATGTCAACAG 592
DB 101 LysIleGlnThrIleGlnLyCyShISlys 110

RESULT 3

ID	Q41829	PRELIMINARY;	PRT;	273 AA.
AC	Q41829;			
DT	01-NOV-1996 (TREMBLrel. 01; Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	MADS box protein.			
GN	ZAP1.			
OS	Zea mays (Maize).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;			
OC	Panicoidae; Andropogoneae; Zea.			
OC	NCBI_TaxID=4577;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=FEMALE INFLORESCENCE;			
RC	MEDLINE=96132144; PubMed=8580958;			
RA	Mena M., Mandel M.A., Lerner D.R., Yanofsky M.F., Schmidt R.J.;			
RT	"A characterization of the MADS-box gene family in maize."			
RT	Plant J. 8:845-854(1995).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.			
DR	EMBL; U46400; AAB00081.1; -			
DR	HSSP; P11831; 1SRS.			
DR	InterPro: IPR002487; TF_Kbox.			
DR	InterPro: IPR002100; TF_MADSbox.			

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 24, 2003, 14:06:48 ; Search time 48 Seconds

(without alignments)
5091.081 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 1030
Sequence: 1 ccggctgcaccagctcgcg.....catacaaaatgtcacaagc 593

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

arched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=x1p
-O=/cgn2.1/USPTO.spool/US10020338/funat.24062003.102354.21507/app.query.fasta_1.775
-DB=SPRMBL.21 -GFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US10020338 @CGN.1.1.138 @funat.24062003.102354.21507 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPELLOCK=100 -LONGLOG
-DEVT_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -RGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

SPRMBL.21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	566	55.0	276	10	Q9LEI0	Q9LEI0 hordeum vul

2	565	54.9	261	10	Q9ZT76	Q9ZT6 lollum temu
3	561	54.5	277	10	Q41829	Q41829 zea mays (m
4	557	54.1	267	10	Q9XJ63	Q9XJ63 oryza sativ
5	557	54.1	267	10	Q9SEW9	Q9SEW9 oryza sativ
6	554	53.8	270	10	Q9FER4	Q9FER4 zea mays (m
7	549	53.3	267	10	Q947B8	Q947B8 oryza sativ
8	539	52.3	228	10	Q04068	Q04068 sorghum bic
9	515	50.0	246	10	Q9MAY7	Q9MAY7 oryza sativ
10	507	49.2	245	10	Q9ZT77	Q9ZT77 lollum temu
11	507	49.2	246	10	Q9SEW0	Q9SEW0 oryza sativ
12	505	49.0	246	10	Q9M7C6	Q9M7C6 oryza sativ
13	503	48.8	244	10	Q82128	Q82128 ericicum ae
14	484	47.0	244	10	Q9LEI2	Q9LEI2 hordeum vul
15	446	43.3	243	10	Q93939	Q93939 betula verr
16	445	43.2	240	10	Q948U1	Q948U1 magnolia pr
17	441	42.8	240	10	Q9AR13	Q9AR13 pismum sativ
18	440	42.7	247	10	Q9SNX1	Q9SNX1 dendrobium
19	437	42.4	239	10	Q82695	Q82695 malus domes
20	433	42.0	248	10	Q8742	Q8742 antirrhinum
21	428	41.6	254	10	Q9XEL0	Q9XEL0 sinapis alb
22	428	41.6	256	10	Q96356	Q96356 brassica ol
23	424	41.2	251	10	Q9SEG1	Q9SEG1 arabidopsis
24	421	40.9	242	10	Q9XHR8	Q9XHR8 nicotiana t
25	421	40.9	252	10	Q941M9	Q941M9 antirrhinum
26	420	40.8	246	10	Q9SBQ1	Q9SBQ1 petunia hyb
27	420	40.8	256	10	Q96355	Q96355 brassica ol
28	418	40.6	244	10	Q93401	Q93401 betula verr
29	418	40.6	260	10	Q93400	Q93400 betula verr
30	416	40.4	242	10	Q9ZTY2	Q9ZTY2 nicotiana t
31	415	40.3	256	10	Q93971	Q93971 brassica ol
32	415	40.3	257	10	Q41356	Q41356 silene latl
33	413	40.1	205	10	Q9FUI2	Q9FUI2 eucalyptus
34	413	40.1	245	10	Q9ZRA5	Q9ZRA5 malus domes
35	412	40.0	255	10	Q9ZRA5	Q9ZRA5 malus domes
36	410	39.8	244	10	Q9FUI3	Q9FUI3 eucalyptus
37	409	39.7	244	10	Q854L5	Q854L5 lycopersico
38	409	39.7	245	10	Q9ZTY3	Q9ZTY3 nicotiana t
39	408	39.6	245	10	Q9XHR7	Q9XHR7 capiscum an
40	407	39.5	247	10	Q9SEG7	Q9SEG7 capiscum an
41	402.5	39.1	245	10	Q9SBO0	Q9SBO0 petunia hyb
42	402	39.0	246	10	Q41355	Q41355 silene latl
43	401.5	39.0	248	10	Q8XRV0	Q8XRV0 helianthus
44	400	38.8	242	10	Q9XHR6	Q9XHR6 nicotiana s
45	400	38.8	245	10	Q9ATE2	Q9ATE2 petunia hyb

ALIGNMENTS

RESULT 1

ID	Q9LEI0	PRELIMINARY;	PRT;	276 AA.
AC	Q9LEI0;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	MADS-box protein 8.			
GN	M8.			
OS	Hordeum vulgare (Barley).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;			
OC	Triticeae; Hordeum.			
OX	NCBI_Taxid=4513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. ATLAS; TISSUE=FLOWER;			
RX	MEDLINE=20346590; PubMed=10890536;			
RA	Schmitz J., Franzen R., Nguyen T., Garcia-Maroto F., Pozzi C.,			
RA	Salamini F., Rohde W.;			
RT	"Cloning, mapping and expression analysis of six barley MADS-box			
RT	genes";			
RL	Plant Mol. Biol. 42:899-913(2000).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).			
CC	-1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.			

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Db 1 MetGlyArgGlyArgValGluLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 QY 323 TTCTCCAGCGCGCGCAAGCGGCTCCTGAGAAGCGCAAGATCTCCGCTCTGTGAC 382
 Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrGluLeuSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGCTCATGCTCTTCTCCCAAGCAAGCAAGCTTATGAGTACGCCACGAC 442
 Db 41 AlaGluValAlaLeuIleIlePheSerAsnArgGlyLysLeuTyrGluPheCysSerSer 60
 QY 443 TCCGACATGACCAAAATCTTGAAGCTTATGAGCGCTACTCTTATGCT----- 490
 Db 61 SerSerMetLeuArgThrLeuGluArgTyrGlnLysCysAsnTyrGlyAlaProGluPro 80
 QY 491 -----GAAAGGCTCTTATTTCAAGCTGAATCTGAAGTGAAGGAAATTGTCGCCAC 541
 Db 81 AsnValProSerArgGluAlaLeuAlaValGluLeuSerSerGln-----Gln 96
 QY 542 GAATTCAGCAAACTTAAGCGCAAGATTGAGACCATACAAAATGTCACAG 592
 Db 97 GluTyrLeuLysLeuLysGluArgTyrAspAlaLeuGlnArgThrGlnArg 113
 RESULT 15
 AGL9_ARADE
 ID AGL9_ARADE STANDARD; PRT; 250 AA.
 AC Q38694;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AGL9 homolog (OML).
 OS Arabidopsis thaliana (Brassicaceae).
 OC Euphorbiales; Malvaceae; Malvaceae; Malvaceae; Malvaceae;
 OC Euphorbiales; Malvaceae; Malvaceae; Malvaceae; Malvaceae;
 OC Euphorbiales; Malvaceae; Malvaceae; Malvaceae; Malvaceae;
 OC Euphorbiales; Malvaceae; Malvaceae; Malvaceae; Malvaceae;
 OC Euphorbiales; Malvaceae; Malvaceae; Malvaceae; Malvaceae;
 NCBI_Taxid=29714;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94072738; PubMed=8251643;
 RA Lu Z.X., Wu M., Loh C.S., Yeong C.Y., Goh C.J.;
 RT "Nucleotide sequence of a flower-specific MADS box cDNA clone from
 RL orchid.";
 RL Plant Mol. Biol. 23:901-904 (1993).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
 CC DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND WEAKLY IN SEEDS BUT
 CC NOT IN THE COLUMN (GYNOCELIUM).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN MATURE FLOWERS AND NOT IN YOUNG
 CC DEVELOPING INFLORESCENCES OR YOUNG FLORAL BUDS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
 CC
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 CC
 CC EMBL: X69107; CAA48559.1; -
 CC HSPD: P11746; ILMN.
 CC TRANSFAC: T03114; -
 CC InterPro: IPR02487; TF_Kbox.
 CC InterPro: IPR02100; TF_MADSbox.
 CC Pfam: PF00319; SRF-TF; 1.
 CC Pfam: PF01486; K-box; 1.
 CC PRINTS: PR00404; MADSDOMAIN.
 CC SMART: SM00432; MADS; 1.
 CC DR PROSITE: PS00350; MADS_BOX_1; 1.
 CC PROSITE: PS50066; MADS_BOX_2; 1.

KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 MADS.
 FT DOMAIN 96 168 K-BOX.
 SQ SEQUENCE 250 AA; 28770 MW; 01EF94DADC499C41 CRC64;
 Alignment Scores:
 Pred. No.: 7.58e-17 Length: 250
 Score: 308.50 Matches: 62
 Percent Similarity: 76.79% Conservative: 24
 Best Local Similarity: 55.36% Mismatches: 21
 Query Match: 29.95% Indels: 5
 DB: 1 Gaps: 2
 US-10-020-338-8 (1-593) x AGL9_ARADE (1-250)
 QY 263 ATGGGTCGCGCAAGTGCAGCTGATGAGCAAGCAAGATTAATCGCAGTGAC 322
 Db 1 MetGlyArgGlyArgValGluLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 QY 323 TTCTCCAGCGCGCGCAAGCGGCTCCTGAGAAGCGCAAGATCTCCGCTCTGTGAC 382
 Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrGluLeuSerValLeuLysAsp 40
 QY 383 GCGAGGTGCGCGCTCATGCTCTTCTCCCAAGCAAGCAAGCTTATGAGTACGCCACGAC 442
 Db 41 AlaGluValAlaLeuIleIlePheSerAsnArgGlyLysLeuTyrGluPheCysSerSer 60
 QY 443 TCCGACATGACCAAAATCTTGAAGCTTATGAGCGCTACTCTTATGCT-----GAAAG 496
 Db 61 SerSerMetLeuArgThrLeuGluArgTyrGlnLysCysAsnTyrGlyAlaProGluPro 80
 QY 497 GCTTTATTTCAAGCTGAATCTGAAGGAAATTGTCGCCACGATACGAGAACTT 556
 Db 81 ThrIleSerArgGluThrGlnSerSerGln-----GlnGluTyrLeuLysLeu 97
 QY 557 AAGCGCAAGATTGAGACCATACAAAATGTCACAG 592
 Db 98 LysAsnArgValGluAlaLeuGlnArgSerGln 109

Search completed: June 24, 2003, 14:12:49
 Job time : 16 secs

RESULT	14			
ID	AGL9_ARATH	STANDARD;	PRT;	251 AA.
AC	022456;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Agamous-like MADS box protein AGU9.			
GN	AGU9 OR AT1G24260 OR F316.19.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eumaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucotsids II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Landsberg erecta;			

US-10-020-338-8 (1-593) x AGL9_ARATH (1-251)

QY 263 ATGGGTCGGCGCAGCTGCACTGAACCGGATAGAGAAACAAGATTAATCCGCGAGTGACC 322

```

Db 1 MetGlyArGlyArValGluLeuLysArgIleGluAsnLysIleAsnArgIValThr 20
Qy 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAAGAGCGCAAGATCTCGTCTGTGAC 382
Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrGluLeuSerValLeuCysAsp 40
Qy 383 GCGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTTATAGTACGCCACGAC 442
Db 41 AlagIValAlaLeuIleValPheSerAsnArgGlyLysLeuTyrGluPheCysSerThr 60
Qy 443 TCCAGCATGACAAATTTCTTAAGCTATAGCGCTACTCTTATGCTGAAAGGCTCTT 502
Db 61 SerAsnMetLeuLysThrLeuGluLysArgTyrGluLysCysSerTyrGlySerIleGluVal 80
Qy 503 ATTTCAGTCGATCGAAGTGAAGTGAAGTATGCTCCAGCATACAGAACTTAAGCGC 562
Db 81 AsnAsnLysProAlaLysGluLeuGluLysAsnSerTyrArgIuTyrLeuLysLeuLysGly 100
Qy 563 AAGATTGAGACCATACAAAAA 583
Db 101 ArgTyrGluAsnLeuGlnArg 107

RESULT 12
AGL9_LYCES
ID AGL9_LYCES STANDARD; PRT; 224 AA.
AC 042464;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (TMS).
GN TMS.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4081;
CX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. VENT Cherry; TISSUE=flower;
RC MEDLINE=93251098; PubMed=1688249;
RA Punell L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA Lifschitz E.;
RT "The MADS box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RT homeotic genes from Antirrhinum and Arabidopsis.";
RL Plant J. 1:255-266(1991).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL; X60758; CAA43170.1; -
DR EMBL; X60480; CAA43010.1; -
DR HSSP; P11746; IANM.
DR TRANSFAC; T03187; -
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.

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DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
DR KX Transcription regulation; DNA-binding; Nuclear.protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 98 170 K-BOX.
SQ SEQUENCE 224 AA; 25999 MW; 51D10D30867D06F7 CRC64;

Alignment Scores:
Pred. No.: 1,04e-17 Length: 224
Score: 319.50 Matches: 66
Percent Similarity: 76.58% Conservative: 19
Best Local Similarity: 59.46% Mismatches: 25
Query Match: 31.02% Indels: 1
DB: 1 Gaps: 1

US-10-020-338-8 (1-593) x AGL9_LYCES (1-224)
Qy 263 ATGGGTGCGCGCAAGGTGACCTGAAGCGATAGAGAACAAATTCGACGTGAC 322
Db 1 MetGlyArGlyArValGluLeuLysArgIleGluLysIleAsnArgIValThr 20
Qy 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAAGAGCGCAAGATCTCGTCTGTGAC 382
Db 21 PheAlaLysArgArgAsnGlyLeuLeuLysLysAlaTyrGluLeuSerValLeuCysAsp 40
Qy 383 GCGAGGTGCGCGTCATCGTCTTCTCCCAAGGCAAGCTTATAGTACGCCACGAC 442
Db 41 AlagIValAlaLeuIleValPheSerAsnArgGlyLysLeuTyrGluPheCysSerThr 60
Qy 443 TCCAGCATGACAAATTTCTTAAGCTATAGCGCTACTCTTATGCTGAAAGGCTCTT 499
Db 61 SerAsnMetLeuLysThrLeuGluLysArgTyrGluLysCysSerTyrGlySerIleGluVal 80
Qy 500 CTTATTCAGTCGATCGAAGTGAAGTGAAGTATGCTCCAGCATACAGAACTTAAG 559
Db 81 AsnLysSerThrArgGluAlaLeuGluLysSerSerGlnGlnTyrLeuLysLeuLys 100
Qy 560 GCGAAGATTGAGACCATACAAAAATGTCACAA 592
Db 101 GlyArgTyrGluAlaLeuGlnArgSerGlnArg 111

RESULT 13
AGL9_SINAP
ID AGL9_SINAP STANDARD; PRT; 254 AA.
AC 004067;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL9 homolog (MADS D).
GN AGL9.
OS Sinapis alba (White mustard) (Brassica hirta).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustroids II; Brassicales; Brassicaceae; Sinapis.
OC NCBI_TaxID=3728;
CX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=flower;
RC MEDLINE=97390682; PubMed=9247539;
RA Bonhomme F., Sommer H., Bernier G., Jacquard A.;
RT "Characterization of SAMDS D from Sinapis alba suggests a dual
RT function of the gene: in inflorescence development and floral
RT organogenesis.";
RL Plant Mol. Biol. 34:573-573(1997).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
CC DEVELOPMENT AND FLORAL ORGANOGENESIS.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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DR TRANSFAC; T03024; -
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3
 FT SEQUENCE 248 AA; 169 K-BOX. 8870DD4512AC906B CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 6.65e-18 Length: 248
 Score: 322.00 Matches: 63
 Percent Similarity: 78.50% Conservative: 21
 Best Local Similarity: 58.88% Mismatches: 23
 Query Match: 31.26% Indels: 0
 Gaps: 0
 US-10-020-338-8 (1-593) x AG14_ARATH (1-248)
 QY 263 ATGGGTCCGCGCAAGTGCAGCTGAGCGAGATAGAGACAAGATTAATCGCAGGTGAC 322
 Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLeuLysIleAsnArgGlnValThr 20
 QY 323 TTCTCCAGCGCCGCGACCGGCTCCTGAGAGAGCGCAGAGATCTCCGTCCTGTGAC 382
 Db 21 PheAlaLysArgArgGlnGlyLeuLeuLysLysAlaTyrGlnLeuSerValLeuLysAsp 40
 QY 383 GCGAGGTCCGCGGTATGCTCTTCCGCCAAAGCAGCTTATGATAGACCCACGAC 442
 Db 41 AlaGlnValAlaLeuLeuIleLeuPheSerAsnArgGlyLysLeuTyrGlnPheCysSer 60
 QY 443 TCCAGCATGACAAATCTTGAAGCTATGAGCGCTACTTATGCTGAAGAGGCTCTT 502
 Db 61 SerAsnMetLeuLysThrLeuAspArgTyrGlnLysCysSerTyrGlySerIleGlnVal 80
 QY 503 ATTTCAGCTGAATCTGAAGAGTGAAGGAATTGGTCCAGCATACAGAAACTTAAGCG 562
 Db 81 AsnAsnLysProAlaLysGlnLeuGlnLysSerTyrArgGlnTyrLeuLysLeuLysGly 100
 QY 563 AAGATTGAGACCATCAAAA 583
 Db 101 ArgTyrGlnAsnLeuGlnArg 107
 SUIT 11
 ID AG14_ARATH STANDARD; PRT; 250 AA.
 AC P29384;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AG14.
 GN AG14 OR AT3G02310 OR F1P3.4.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RX SEQUENCE FROM N.A.
 RX MEDLINE=91160981; PubMed=1672119;
 RA Ma H., Yanofsky M.F., Meyerowitz E.M.;
 RT "AG14-AG16, an Arabidopsis gene family with similarity to floral
 RT homeotic and transcription factor genes.";
 RL Genes Dev. 5:484-495(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;

RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unselid M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
 RA Delzeny M., Boutry M., Griveill L.A., Maché R., Pigdemmech P.,
 RA De Simone V., Choisne N., Arriguenave F., Robert C., Brotier P.,
 RA Wincker P., Catellio L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Muller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wumbach E., Dizonok H., Eflie H., Jordan N., Bangert S.,
 RA Widelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simonetti B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.H., Norisiek G.,
 RA Reichelt J., Scharte M., Schoen O., Barques M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
 RA Cooke R., Lande M., Berger-Llauro C., Purnelle B., Masny D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cortet A., Casacuberta E.,
 RA Monfort A., Argirion A., Flores R., Lignori R., Vitale D.,
 RA Mannheim G., Haase D., Schoof H., Radd S., Zaccaria P., Wewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Talion L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walte A., Utecherback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Maltl R., Wu D., Peterson J., Van Aken S.,
 RA Pail G., Miltischer J., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
 RA Sasaomoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:820-822(2000).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING FLOWER DEVELOPMENT.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
 CC
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 CC
 DR EMBL; M55552; AAA32734.1; -
 DR EMBL; AC009755; AAF02125.1; -
 DR PIR; D39534; D39534.
 DR HSSP; P11746; IMM.
 DR TRANSFAC; T03027; -
 DR InterPro: IPR002487; TF_Kbox.
 DR InterPro: IPR002100; TF_MADSbox.
 DR Pfam; PF00319; SRF-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 DR Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3
 FT SEQUENCE 250 AA; 169 K-BOX. 53136FE26338943 CRC64;
 SQ
 Alignment Scores:
 Pred. No.: 6.65e-18 Length: 250
 Score: 322.00 Matches: 64
 Percent Similarity: 78.50% Conservative: 20
 Best Local Similarity: 59.81% Mismatches: 23
 Query Match: 31.26% Indels: 0
 Gaps: 0
 US-10-020-338-8 (1-593) x AG14_ARATH (1-250)
 QY 263 ATGGGTCCGCGCAAGTGCAGCTGAGCGAGATAGAGACAAGATTAATCGCAGGTGAC 322

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OY 333 GCGAGAGTCGCGCGATCTCTCTTCTCCGCCAAGGACACTATGATGACGACCGAC 442
Db 41 AlagIvalAlAlbLeuIleValIhPheSerAsnAGGlyLysLeuIlycIunPheCysSerThr 60
OY 443 TTCACGATGACCAAAATTCCTTGAACGTTATYAGAGCGCTACTCTTATGCTGAAAGGCTCTT 502
Db 61 SerCysMetAsnLysThrLeuGlnIuArgIyTyrGlnIuArgCysSerTyrGlySerLeuGlnThr 80
OY 503 ATTGACGCTGATCTGAAGATGAGGGAATTTGGTGCACGATATACAGAACTTAAAGCG 562
Db 81 SerGlnProSerLysGlnIuThrIuNbsSerTyr--GlnIuIyIleuNysLeuNysAla 99
OY 563 AAGATTGAGACCATCAAAAATGTCACAAAG 592
Db 100 LysValAspValLeuGlnIuArgSerHisArg 109

RESULT 9
AGL9_PETHY STANDARD; PRT; 241 AA.
003489;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Agamous-like MADS box protein AGL9 homolog (floral homeotic protein
FBP2). (Floral binding protein 2).
DE FBP2.
GN
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxId=4102;
[1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=93005737; PubMed=1356537;
RA Angenent G.C.; Buschacher M.; Franken J.; Mol J.N.M.; van Tunen A.J.;
RT "Differential expression of two MADS box genes in wild-type and
RT mutant petunia flowers.";
RL Plant Cell 4:983-993(1992).
[2]
RN
RP REVISIONS TO C-TERMINUS.
RA Angenent G.C.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC
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CC
CC EMBL; M91666; AAA86854.1; -.
CC PIR; J01690; J01690.
CC HSSP; P11746; 1NMN.
CC TRANSFAC; T03093; -.
CC InterPro; IPR002487; TF_Kbox.
CC InterPro; IPR002100; TF_MADSbox.
CC Pfam; PF00319; SRF-TF; 1.
CC Pfam; PF01486; K-box; 1.
CC PRINTS; PR00404; MADSDOMAIN.
CC SMART; SM00432; MADS_1.
CC PROSITE; PS00350; MADS_BOX_1; 1.
CC PROSITE; PS50066; MADS_BOX_2; 1.
CC Trnscriptipion regulation; DNA-binding; Nuclear protein.
CC DOMAIN 3 57 MADS.
CC FT DOMAIN 98 170 K-BOX.
CC SEQUENCE 241 AA; 27562 MW; B575BB946BD310BB CRC64;

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Alignment Scores:
Pred. No.: 1 43e-18      Length: 241
Score: 330.50      Matches: 68
Percent Similarity: 78.38%      Conservative: 19
Best Local Similarity: 61.26%      Mismatches: 23
Query Match: 32.09%      Indels: 1
DB: 1      Gaps: 1

US-10-020-338-8 (1-593) x AGL9_PETHY (1-241)

QY 263 ATGGGTGGCGGCGACGTGACAGCTGAAACGGATGAGAACAGATAAATCGGACGTGACC 322
Db 1 MccIyargtgyarValGtuleuLyarGtlleuLmLyrsIleAenArGlnValThr 20
QY 323 TTCTCCAAAGCGCCGCAACGGGCTCTCTGAAGAAGCGCACAGATCTCCGCTTGAGAC 382
Db 21 PheIalysArGArGaenGlyLeuLeuLyelysAlarYrGluLeuSerValIeuCyasp 40
QY 383 GCGGAGGTGCGCGGATCGCTCTCTCCCAAGGCAAGCTATAGTAGTACGCCACCGAC 442
Db 41 AlaIuValAlaLeuIleIlePheSerAsnArgGlyLysLeuYrGluIueCySerSer 60
QY 443 TCCAGCATGACAAAAATTTCTGGAACGTTATAGAGCGCTACTCTTAT--GCTGAAGAAGCT 499
Db 61 SerSerIeuLysrThrIeuLysrGluArGtYrGlnLysCySerAsnYrGlyAlaProGluThr 80
QY 500 CTATTTACCTGCTGAATCTGAAAGTGAGGGAATTGGTCCACAGATACAGGAACTTAA 559
Db 81 AsnIleSerThrArGlnAlaLeuGlnIleLeuSerGlnGlnGluYrLeuLys 100
QY 560 GCGAAGATTGAGACCATACAAAATGTGCACAG 592
Db 101 AlaArgYrGluAlaLeuGlnArgSerGlnArg 111

RESULT 10
AGL2_ARATH
ID AGL2_ARATH STANDARD; PRT; 248 AA.
AC P29382;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AGL2.
GN AGL2
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91160981; PubMed=1672119;
RA Ma H., Yancovsky M.F., Meyerowitz E.M.;
RT AGL1-AG6, an Arabidopsis gene family with similarity to floral
RT homeotic and transcription factor genes."
RL Genes Dev. 5:484-495(1991).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC
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CC
DR EMBL; M55551; AAA37732.1; -
DR PIR; B39534; B39534.
DR HSP; P11746; IWMN.

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RP FUNCTION, AND TISSUE SPECIFICITY.
RC STRAIN=cv. Landsberg erecta;
RX MEDLINE=98171466; PubMed=9502732;
RA Gu Q., Ferrandiz C., Yanofsky M.F., Marcussen R.;
RT "The FRUITFULL MADS-box gene mediates cell differentiation during
RL Arabidopsis fruit development."; Development 125:1509-1517(1998).
CC -1- FUNCTION: Probable transcription factor required for normal
CC pattern of cell division, expansion and differentiation during
CC morphogenesis of the silique.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: Vascular tissue of cauline leaves, floral
CC shoot apex and valves of carpels and fruits.
CC -1- INDUCTION: Dramatically up-regulated upon the transition from
CC vegetative to reproductive development.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL, U33473; AAA97403.1; -;
DR EMBL, AB008269; BAB10640.1; -;
DR EMBL, AF386929; AAK62374.1; -;
DR EMBL, AY072463; AAL66878.1; -;
DR HSSP; P11746; IMM.
DR TRANSFAC; T03030; -;
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 242 AA; 27536 MW; 51649931EADB2D2 CRC64;

Alignment Scores:
Pred. No.: 6.2e-24 Length: 242
Score: 399.00 Matches: 75
Percent Similarity: 85.98% Conservative: 17
Best Local Similarity: 70.09% Mismatches: 15
Query Match: 38.74% Indels: 0
DB: 1 Gaps: 0
US-10-020-338-8 (1-593) x AGL8_ARATH (1-242)
OY 263 ATGGGTCCGCGCAAGTGTGACGATGAGCAAGATTAATTCGGACGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThr 20
OY 323 TTCTCCAGAGCGCGCAAGCGGCTCTGAAAGAGCGACGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgSerCylLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
OY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCAAGGCAAGCTTATGATGACCGAC 442
DB 41 AlaGluValAlaLeuIleValPheSerSerLysGlyLysLeuPheGluLysSerThrAsp 60
OY 443 TCCACAGAGCAAAATCTTGAACGTATGAGCGCTACTCTTATGCTGAAAGGCTCTT 502
DB 61 SerCysMetGluArgIleLeuGlnLysArgIleValPheArgLysLeuLysSerValLeuLys 80
OY 503 ATTGAGGTGATCGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGCG 562

DB 81 ValGlyArgAspValSerGlnSerGlnAsnTriPValLeuGlnHISAlaLysLeuLysAla 100
OY 563 AAGATTGAGACCATACAAAA 583
DB 101 ArgValGluValLeuGlnLys 107
RESULT 8
CMBL_DIACA
ID CMBL_DIACA STANDARD; PRT; 233 AA.
AC Q3685;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE MADS box protein CMBL.
GN CMBL.
OS Dianthus caryophyllus (Carnation) (Clove pink).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Caryophyllaceae; Dianthus.
OX NCBI_TaxID=3570;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Scania; TISSUE=Petal;
RA Baudinette S.C., Savin K.W.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL; L40404; AAA62761.1; -;
DR HSSP; P11746; IMM.
DR TRANSFAC; T03060; -;
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS50066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 58 MADS.
FT DOMAIN 96 168 K-BOX.
SQ SEQUENCE 233 AA; 26888 MW; CB8765618466151A CRC64;

Alignment Scores:
Pred. No.: 2.26e-20 Length: 233
Score: 353.50 Matches: 69
Percent Similarity: 80.00% Conservative: 19
Best Local Similarity: 62.73% Mismatches: 21
Query Match: 34.32% Indels: 1
DB: 1 Gaps: 1
US-10-020-338-8 (1-593) x CMBL_DIACA (1-233)
OY 263 ATGGGTCCGCGCAAGTGTGACGATGAGCAAGATTAATTCGGACGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThr 20
OY 323 TTCTCCAGAGCGCGCAAGCGGCTCTGAAAGAGCGACGAGATCTCCGCTCTGTGAC 382
DB 21 PheAlaLysArgArgGlnGlyLeuLeuLysLysAlaLysArgIleGlnLysSerValLeuLysAsp 40

QY 363 GCGAGGTGCGCGTATGCTTTCTCCCAAGGACGCTTATGATGACGCCACGAC 442
 DB 41 AlagluvalalgluvalaleuvalpheserthylslylsleuPhesglutylalalaasnap 60
 QY 443 TCCAGCATGACAAATTTGATGAGCGCTACTCTTATGCTGAAAGGCTCTT 502
 DB 61 SerCysmetgluargluvalgluarglyserPhesglutylalalaasnap 80
 QY 503 ATTGAGCTGATGAAATGAGGAAATGAGCGCTGCAATGACGAACTTAAGGCG 562
 DB 81 ValProthAspHisThrSerProglYserTrpThrleuGluHisAlaIysleuysAla 100
 QY 563 AAGATTGAGACCATACAAAATGTCACAG 592
 DB 101 ArgleuGluValleuGlnArgAsnGlnlys 110
 RESULT 6
 AGL8_SINL STANDARD; PRT; 241 AA.
 ID AGL8_SINL Q41274;
 AC 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AGL8 homolog (MADS B).
 GN AGL8.
 OS Sinapis alba (White mustard) (Brassica hirta).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Sinapis.
 OX NCBI_TaxID=3728;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=flower;
 RX MEDLINE=97077349; PubMed=8919916;
 RA Menzel G., Apel K., Melzer S.;
 RT "Identification of two MADS box genes that are expressed in the
 RT apical meristem of the long-day plant Sinapis alba in transition to
 RT flowering.";
 RL Plant J. 9:399-408(1996).
 CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN APICAL MERISTEMS IN TRANSITION
 CC TO FLOWERING.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTRAINS 1 K-BOX DIMERIZATION DOMAIN.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; U25695; AAB41525.1; -
 DR HSSRP; P11746; 1MMN.
 DR TRANSFAC; T03168; -
 DR InterPro; IPR002487; TF_Kbox.
 DR InterPro; IPR002100; TF_MADSbox.
 DR Pfam; PF03119; SRF-TF; 1.
 DR Pfam; PF01486; K-box; 1.
 DR PRINTS; PR00404; MADSDOMAIN.
 DR SMART; SM00432; MADS; 1.
 DR PROSITE; PS00350; MADS_BOX_1; 1.
 DR PROSITE; PS50066; MADS_BOX_2; 1.
 RT Transcription regulation; DNA-binding; Nuclear protein.
 FT DOMAIN 3 MADS.
 FT SEQUENCE 241 AA; 27660 MW; 06626CC598EA94A9 CRC64;
 Alignment Scores: 5.18e-24 Length: 241
 Pred. No.:

Score: 400.00 Matches: 74
 Percent Similarity: 85.98% Conservative: 18
 Best Local Similarity: 69.16% Mismatches: 15
 Query Match: 38.93% Indels: 0
 DB: 1 Gaps: 0
 US-10-020-338-8 (1-593) x AGL8_SINL (1-241)
 QY 263 ATGGGTGCGCGCAAGTGCACCTGAAGCGGATGAGAAACAGATTAATCGCAGGTGACC 322
 DB 1 MetGlyArgGlyArgValGlnleuYserGlyleuGluValleuYserValleuYserThrAsp 20
 QY 323 TTCTCCAGCGCGCGCAAGCGGCGCTCTGAAAGGCGCAGAGATCTCCGCTCTGTGAC 382
 DB 21 PheSerlyAsArgAsGserGlyleuYserGlyleuYserAlaHisGlyIleSerValleuYserAsp 40
 QY 383 GCGAGGTGCGCGCTATGCTTTCTCCCAAGGACGCTTATGATGACGCCACGAC 442
 DB 41 AlagluvalalaleuvalleuPheserthylslylsleuPhesglutylalalaasnap 60
 QY 443 TCCAGCATGACAAATTTGATGAGCGCTACTCTTATGCTGAAAGGCTCTT 502
 DB 61 SerCysmetgluargluvalgluarglyserPhesglutylalalaasnap 80
 QY 503 ATTGAGCTGATGAAATGAGGAAATGAGCGCTGCAATGACGAACTTAAGGCG 562
 DB 81 ValGlyArgAspHisThrSerProglYserTrpThrleuGluHisAlaIysleuysAla 100
 QY 563 AAGATTGAGACCATACAAAATGTCACAG 592
 DB 101 ArgValGluValleuGlnArg 107
 RESULT 7
 AGL8_ARATH STANDARD; PRT; 242 AA.
 ID AGL8_ARATH Q38876;
 AC 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agamous-like MADS box protein AGL8 (Floral homeotic protein AGL8)
 DE (FRUITFULL).
 GN AGL8 OR FUL OR AT5G60910 OR MSL3.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=96093419; PubMed=8535133;
 RA Mandel M.A., Yanofsky M.F.;
 RT "The Arabidopsis AGL8 MADS box gene is expressed in inflorescence
 RT meristems and is negatively regulated by ADELAYAL.";
 RL Plant Cell 7:1763-1771(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=96162728; PubMed=9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned P1 clones.";
 RL DNA Res. 4:401-414(1997).
 RN (3)
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC).";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN (4)

OX NCBI_TaxID=4081;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=cv. VENT Cherry; TISSUE=Flower;
RX MEDLINE=93251098; PubMed=1688249;
RA Pnueli L., Abu-Abeid M., Zamir D., Nacken W., Schwarz-Sommer Z.,
RA Lifschitz E.;
RT "The MADS box gene family in tomato: temporal expression during
RT floral development, conserved secondary structures and homology with
RT homeotic genes from Antirrhinum and Arabidopsis.";
RL Plant J. 1:255-266(1991).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: Flower-specific.
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL; X60757; CAA43169.1; -
DR HSSP; P11746; IMNM.
DR TRANSFAC; T03186; -
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 227 AA; 26403 MW; 4976195B3BDE53F5 CRC64;

Alignment Scores:
Pred. No.: 1,22e-24 Length: 227
Score: 408.00 Matches: 79
Percent Similarity: 85.45% Conservative: 15
Best Local Similarity: 71.82% Mismatches: 16
Indels: 0
Query Match: 1 Gaps: 0

US-10-020-338-8 (1-593) x AG18_LYCS (1-227)
OY 263 ATGGGTGCGGCGAGTGCAGCTGAGCGATAGAGAAAGATTAATCGCAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysValIleAsnArgGlnValThr 20
OY 323 TTCTCAAGCCCGCGAAGCGGCTCTGAAAGAGCGACGAGATCTCGTCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
OY 383 GCGAGAGTGCAGCGATGCTTCTCCCGCAAGGACGCTATAGAGAGCGACGAC 442
DB 41 AlaGlnValGlyLeuIleValPheSerThrLysGlyLysLeuPheGlnLysIleAsnAsp 60
OY 443 TTCACATGACCAAAATTTCTTAACGTTATGAGCGCTACTTATGCTGAAAAGCTCTT 502
DB 61 SerCysMetGluArgIleLeuGlnLysArgLysArgLysSerPheAlaGlnLysGlnLeu 80
OY 503 ATTGACGCTGATCTGAAGAGTGAAGGAAATTTGCTCCACGATACAGGAAATTTAAGCG 562
DB 81 ValProThrAspHisThrSerProValSerThrPheLeuGlnLysAlaArgLysLeuLysAla 100
OY 563 AAGATTGAGACCATCAAAATATGTCACAAG 592

DB 101 ArgLeuGlnValLeuGlnArgGlnGlnLys 110
RESULT 5
ID AG18_SOLITU STANDARD; PRT; 250 AA.
AC 042429;
DT 15-DEC-1998 (Rel. 37, Last Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Agamous-like MADS box protein AG18 homolog (POTM1-1).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Superior;
RX MEDLINE=96343939; PubMed=8756601;
RA Kang S.G., Hannapel D.J.;
RT "A novel MADS-box gene of potato (Solanum tuberosum L.) expressed
RT during the early stages of tuberization.";
RL Plant Mol. Biol. 31:379-386(1996).
CC -1- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC -1- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
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CC -----
DR EMBL; U23758; AAA92840.1; -
DR EMBL; U23757; AAA92839.1; -
DR HSSP; P11746; IMNM.
DR TRANSFAC; T03145; -
DR InterPro; IPR002487; TF_Kbox.
DR InterPro; IPR002100; TF_MADSbox.
DR Pfam; PF00319; SRF-TF; 1.
DR Pfam; PF01486; K-box; 1.
DR PRINTS; PR00404; MADSDOMAIN.
DR SMART; SM00432; MADS; 1.
DR PROSITE; PS00350; MADS_BOX_1; 1.
DR PROSITE; PS00066; MADS_BOX_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein.
FT DOMAIN 3 57 MADS.
FT DOMAIN 97 169 K-BOX.
SQ SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4 CRC64;

Alignment Scores:
Pred. No.: 1.76e-24 Length: 250
Score: 406.00 Matches: 77
Percent Similarity: 85.45% Conservative: 17
Best Local Similarity: 70.00% Mismatches: 16
Indels: 0
Query Match: 1 Gaps: 0

US-10-020-338-8 (1-593) x AG18_SOLITU (1-250)
OY 263 ATGGGTGCGGCGAGTGCAGCTGAGCGATAGAGAAAGATTAATCGCAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysValIleAsnArgGlnValThr 20
OY 323 TTCTCAAGCCCGCGAAGCGGCTCTGAAAGAGCGACGAGATCTCGTCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40

DR	PROSITE; PS50066; MADS_BOX_2; 1.
KM	Transcription regulation; DNA-binding; Activator; Nuclear protein.
KW	Developmental protein; Polymorphism.
FT	DOMAIN 3 MADS. 57
FT	DOMAIN 97 K-Box.
FT	VARIANT 85 S -> P (IN STRAIN CV. BLA-1).
FT	VARIANT 85 M -> T (IN STRAIN CV. BLA-1).
FT	VARIANT 93 S -> T (IN STRAIN CV. BLA-1).
FT	VARIANT 99 K -> R (IN STRAIN CV. CHI-1).
FT	VARIANT 100 A -> T (IN STRAIN CV. IER).
FT	VARIANT 120 M -> V (IN STRAIN CV. DL-1).
FT	VARIANT 125 L -> P (IN STRAIN CV. BLA-1).
FT	VARIANT 166 S -> G (IN STRAIN CV. DL-1).
FT	VARIANT 212 L -> P (IN STRAIN CV. BLA-1).
FT	VARIANT 233 L -> V (IN STRAIN CV. CHI-1).
FT	CONFLICT 184 E -> G (IN REF. 3; AAM28458).
FT	CONFLICT 236 MISSING (IN REF. 1).
SQ	SEQUENCE 256 AA; 30182 MW; 01EB26B1ECB3476C CRC64;

Alignment Scores:	
Read No.:	6,85e-26
Score:	424.00
Percent Similarity:	88.79%
Best Local Similarity:	76.64%
Query Match:	41.17%
DB:	1
Length:	256
Matches:	13
Conservative:	82
Mismatches:	12
Indels:	0
Gaps:	0

US-10-020-338-8 (1-593) x API_ARATH (1-256)

[illegible]

db 101 LysIleGluLeuGluArg 107

db 101 LysIleGluLeuGluArg 107

RESULT 3

```

AGL8_SOLCO
ID_AGL8_SOLCO
STANDARD;
PRT; 250 AA.

```

DT 15-DEC-1998 (Rel. 37, Created)

DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)

Agamous-like MADS box protein AGL8 homolog.
SCM1.

OS solanum commersonii (Commerson's wild potato
OC Eukaryota; Viridiplantae; Streptophyta; Embry

OC Spermatophyta; Magnoliophyta; eudicotyledons
OC Asteridae; euasterids I; Solanales; Solanaceae

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OX NCBI_TAXID=4109;
RN [1]

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RP SEQUENCE FROM N.A.
RA Seppanen M.M.;

Submitted (MAY-1997) to the EMBL/GenBank/DD

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity)
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY

```

CC      FACTORS.
CC      -i- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN

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CC	EMBL; AF002666; AAB65161.1; -.
DR	HSSP; P11746; 1MM.
DR	InterPro; IPR002487; TF_Kbox.
DR	InterPro; IPR002100; TF_MADSbox.
DR	Pfam; PF00319; SRF-TF; 1.
DR	Pfam; PF01486; K-box; 1.
DR	PRINTS; PR00404; MADSDOMAIN.
DR	SMART; SM00432; MADS; 1.
DR	PROSITE; PS00350; MADS_BOX_1; 1.
DR	PROSITE; PS50066; MADS_BOX_2; 1.
KW	Transcription regulation; DNA-binding; Nuclear protein
FT	DOMAIN 3 57 MADS.
FT	DOMAIN 97 169 K-BOX.
SQ	SEQUENCE 250 AA; 28741 MW; C9871403C23ED5D5 CR664;

Alignment Scores:	
Pred. No.:	8.55e-25
Score:	410.00
Percent Similarity:	85.45%
Best Local Similarity:	71.82%
Query Match:	39.81%
DB:	1
Gaps:	0
Length:	250
Matches:	79
Conservative:	15
Mismatches:	16
Indels:	0
Gaps:	0

US-10-020-338-8 (1-593) X AGL8_SOLCO (1-250)

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Oy      263  ATGGAGTCGGGAGAGGTGCAGCTGAAAGCGGATTAAGAAACAAGATAATTCGGACAGGTGACC 332
Db      1  MetGlyArgGlyArgValGlnLeuLeuArgTgIleGlnuInuYsIleAsnAArgGlnValThr 20

Oy      323  TTCTCCAAAGCGCGGCAACGGAGCTCTGTGAAGAAGCGGACAGAGATCTTCGGTCTCTGTGAC 382
Db      21  PheSerLysArgArgSerGlyLeuLeuLeuLysAlaIleGlnIleSerValLeuGlyAsp 40

Oy      383  GCGGAGGTGCGCGTATGCTCTTCTTCCCGCAAGCGAAGCTCTATAGTACGGCACCGAC 442
Db      41  AlaGluValGlyLeuIleValPheSerThrLysGlyLysLeuPheGlnTyrAlaIleThrAsp 60

Oy      443  TTCAGCATGGAACAAATCTTGAACGGTATAGAGGCGTATCTTATGCTGAAAAGGCGCTT 502
Db      61  SerCysMetGluArgLeuLeuGlnIleuArgTgIleuArgTgIleuSerPheAlaGlnLysGlnLeu 80

Oy      503  ATTCAGCTGAATCTGAAGAAGTAGAGGAAATTGTCGCCACGAAATCCAGAAATTTAAGCGC 562
Db      81  ValProThrAspPheIleThrSerProGlySerThrPheIleuGlnuAsnAlaIleuLysAla 100

Oy      563  AACATTGAGACCATCAAAAATATGCACAG 592
Db      101  ArgLeuGluValLeuGlnIleArgAsnGlnLys 110

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[illegible]

AGL8 LYC

ID	AGL8_LYCES	STANDARD;	PRT;	227	AA
AC	040170:				

DT	15-DEC-1998 (Rel. 37, Created
DT	15-DEC-1998 (Rel. 37, Last ser

DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Agamous-like MADS box protein AG1.8 homolog

OS Lycopersicon esculentum (Tomato).
GN TDR4.

Eukaryota; Viridiplantae; Streptophyta; Emb
Spermatophyta; Magnoliophyta: eudicotyledon

Asteridae; euasterids I; Solanales; Solanaceae

[illegible]

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 24, 2003, 14:07:53 ; Search time 13 Seconds

(without alignments)
3783.917 Million cell updates/sec

Title: US-10-020-338-8

Sequence: 1 ccggctgcagccagcgtccg.....catacaaaatgctacaagc 593

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Zgapop 6.0, Zgapext 7.0
Delop 6.0, Delext 7.0

arched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2/1/USPTO.spool/US10020338/runat.24062003.102354.21495/app.query.fasta.1.775
-DB=SwissProt 40 -QFMT=fasta -SUFFIX=esp -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10020338 @CGN 1 1 26 @runat.24062003.102354.21495 -NCPU=6 -ICPU=3
-NO MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARR TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	424	41.2	254	1	AP1_SINAI
2	424	41.2	256	1	AP1_ARATH
3	410	39.8	250	1	AGL8_SOLCO
4	408	39.6	227	1	AGL8_LYCES
5	406	39.4	250	1	AGL8_SOLTU
6	400	38.8	241	1	AGL8_SINAI
7	399	38.7	242	1	AGL8_ARATH
8	353.5	34.3	233	1	AGL2_DIACA
9	330.5	32.1	241	1	AGL9_PETHY
10	322	31.3	248	1	AGL2_ARATH
11	322	31.3	250	1	AGL4_ARATH
12	319.5	31.0	224	1	AGL9_LYCES
13	315.5	30.6	254	1	AGL9_SINAI
14	314.5	30.5	251	1	AGL9_ARATH
15	308.5	30.0	250	1	AGL9_ARADE
16	305	29.6	252	1	AGL6_ARATH
17	300	29.1	258	1	AGL3_ARATH
18	279.5	27.1	242	1	AG_PANGI

19	276.5	26.8	214	1	SOC1_ARATH	06465	arabidopsis
20	276.5	26.8	230	1	AGL1_ARATH	Q38836	arabidopsis
21	274.5	26.7	240	1	AGL1_ARATH	P29361	arabidopsis
22	273.5	26.6	264	1	AGL5_BRANA	Q39295	brassica na
23	272.5	26.5	248	1	AGL5_TOBAC	Q43585	nicotiana t
24	269.5	26.2	242	1	AG_PETHY	P29385	petunia hyb
25	269.5	26.2	246	1	AGL5_ARATH	Q38837	arabidopsis
26	267.5	26.0	244	1	AGL4_ARATH	Q38838	arabidopsis
27	267	25.9	221	1	AGL4_ARATH	Q40168	lycopersico
28	266.5	25.9	248	1	AG_LYCES	Q01540	brassica na
29	260.5	25.3	252	1	AG_BRANA	Q38847	arabidopsis
30	260	25.2	268	1	AGL5_ARATH	Q38841	arabidopsis
31	259.5	25.2	211	1	AGL2_ARATH	P17839	arabidopsis
32	259.5	25.2	252	1	AGL_ARATH	Q52176	arabidopsis
33	254	24.7	228	1	AGL1_ARATH	Q34688	arabidopsis
34	252	24.5	210	1	FBP1_PETHY	P48007	arabidopsis
35	247	24.0	209	1	GLOB_TOBAC	Q03416	nicotiana t
36	246.5	23.9	219	1	AG19_ARATH	Q82743	arabidopsis
37	245.5	23.8	178	1	AG31_ARATH	Q95617	arabidopsis
38	237.5	23.1	232	1	AP3_ARATH	P48007	arabidopsis
39	234	22.7	208	1	PIST_ARATH	Q07472	petunia hyb
40	234	22.7	212	1	MAD2_PETHY	Q02078	homo sapien
41	234	22.7	507	1	MEPA_HUMAN	P23706	antirrhinum
42	233.5	22.7	227	1	DEFA_ANTMA	Q03378	antirrhinum
43	233	22.6	215	1	GLOB_ANTMA	Q95747	arabidopsis
44	230.5	22.4	196	1	FLC_ARATH	Q38840	arabidopsis
45	230	22.3	227	1	AG17_ARATH		

ALIGNMENTS

RESULT 1
AP1_SINAI STANDARD; PRT; 254 AA.
AC Q41276:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Floral homeotic protein APTAL1 (VADS C).
GN APT.
OS Sinapis alba (white mustard) (Brassicaceae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Sinapis.
OX NCBI_Taxid=3728;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Flower;
RX MEDLINE=95334514; PubMed=7610185;
RA Menzel G., Apel K., Melzer S.;
RT "Isolation and analysis of SAMDS C, the APTAL1 cDNA homolog from
mustard";
RL plant Physiol. 108:853-854 (1995).
CC -!- FUNCTION: CONTROLS FLORAL MERISTEM IDENTITY. IS ALSO REQUIRED FOR
NORMAL DEVELOPMENT OF SEEDS AND PETALS. IS REQUIRED FOR THE
TRANSLATION OF AN INFLUORESCENCE MERISTEM INTO A FLORAL MERISTEM.
CC INTERACTS WITH LEAFY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
FACTORS.
CC -!- SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: X81480; CA57233.1; --
CC HSP: P11746; IMNM.
CC TRANSFAC: T03169; --

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Oy 563 AAGATGAGACCATACAAATGTCACAG 592
Db 101 ArgLeuGIuValLeuGIuArgAnGIuLys 110

RESULT 7

S23730

MADS box protein TDR4 - tomato

N/Alternate names: floral homeotic protein TM4

C/Species: Lycopersicon esculentum (tomato)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999

C/Accession: S23730

R/Punell, L.; Abu-Abaid, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschitz, E.

Plant J. 1: 255-266, 1991

A/Title: The MADS box gene family in tomato: temporal expression during floral development

A/Reference number: S23728; MUID:93251098; PMID:1688249

A/Accession: S23730

A/Molecule type: mRNA

Residues: 1-227 <PNU>

Cross-references: EMBL:X60757; NID:g19381; PIDN:CAA43169.1; PID:g19382

Genetics:

A/Gene: TDR4

A/Map position: 6

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.:	6.39e-29	Length:	227
Score:	408.00	Matches:	79
Percent Similarity:	85.45%	Conservative:	15
Best Local Similarity:	71.82%	Mismatches:	16
Query Match:	39.61%	Indels:	0
DB:	2	Gaps:	0

US-10-020-338-8 (1-593) x S23730 (1-227)

Oy 263 ATGGGTGCGCGCAAGTGCAGCTGAGGATAGAGCAAGATTAATCGGAGTGACC 322
Db 1 MetGIyArgGIyArgValGIuLeuLysArgIIeGIuAnLysIIeAsnArgGIuValThr 20

Oy 323 TTCTCCAGCGCGCAACGGGCTCTGGAAGAGCGACGAGATCTCCGTCCTGTGAC 382
Db 21 PheSerIySArgIySArgSerGIyLeuLeuLysIySAlaHISGIuIleSerValLeuLysasp 40

Oy 383 GCGAGGTGCGCGATGCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
Db 41 AlaGIuValGIyLeuIleValPheSerThrIySGIyLysLeuPheGIuTyAlaAsnasp 60

Oy 443 TCCAGCATGACAAATTCCTTGAACCTTATGAGCGCTCTTATGCTGAAGGCTTT 502
Db 61 SerCysMetGIuArgIleLeuGIuArgIyGIySerPheAlaGIuLysGIuLeu 80

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 563 AAGATGAGACCATACAAATGTCACAG 592
Db 101 ArgLeuGIuValLeuGIuArgAnGIuLys 110

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

A/Molecule type: mRNA
A/Residues: 1-250 <KAN>
A/Cross-references: EMBL:U23757; NID:g758564; PIDN:AA92839.1; PID:g758565
A/Experimental source: cv. Superior; vegetative tissue; tuber induced 4-day axillary bu
C/Genetics:
A/Gene: POTM1-1
C/Function:
A/Description: may be involved in vegetative organ development of potato
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
C/Keywords: DNA binding; nucleus; transcription factor; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.:	9.84e-29	Length:	250
Score:	406.00	Matches:	77
Percent Similarity:	85.45%	Conservative:	17
Best Local Similarity:	70.00%	Mismatches:	16
Query Match:	39.42%	Indels:	0
DB:	2	Gaps:	0

US-10-020-338-8 (1-593) x T07100 (1-250)

Oy 263 ATGGGTGCGCGCAAGTGCAGCTGAGGATAGAGCAAGATTAATCGGAGTGACC 322
Db 1 MetGIyArgGIyArgValGIuLeuLysArgIIeGIuAnLysIIeAsnArgGIuValThr 20

Oy 323 TTCTCCAGCGCGCAACGGGCTCTGGAAGAGCGACGAGATCTCCGTCCTGTGAC 382
Db 21 PheSerIySArgIySArgSerGIyLeuLeuLysIySAlaHISGIuIleSerValLeuLysasp 40

Oy 383 GCGAGGTGCGCGATGCTCTTCTCCCAAGGCAAGCTTATGAGTACGCCACGAC 442
Db 41 AlaGIuValGIyLeuIleValPheSerThrIySGIyLysLeuPheGIuTyAlaAsnasp 60

Oy 443 TCCAGCATGACAAATTCCTTGAACCTTATGAGCGCTCTTATGCTGAAGGCTTT 502
Db 61 SerCysMetGIuArgIleLeuGIuArgIyGIySerPheAlaGIuLysGIuLeu 80

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 563 AAGATGAGACCATACAAATGTCACAG 592
Db 101 ArgLeuGIuValLeuGIuArgAnGIuLys 110

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Oy 503 ATTCACCTGATCTGAAAGTGAAGGAAATGTGTCCAGATACAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProValSerThrIyPheGIuHisArgIyLeuLysAla 100

Pred. No.: 2.3e-30 Length: 254
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x S52236 (1-254)

QY 263 ATGGGTCCGGCGCAAGTGCAGCTGAGGAGATAGAGAACAGATTAATCGCAGGTGACC 322
Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGGCGCCGCAAGCGGCTCCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgGlyArgValGlnLeuLysLysIleGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGGTCCGCGTATGCTCTTCTCCCGCAAGGCAAGCTCTATGATGACGCCACGAC 442
Db 41 AlaGluValAlaLeuValPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAACGTATGAGCGCTCTTATGCTGAAGAGGCTCTT 502
Db 61 SerCysMetGluLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGTGAAGGAAATTGGTCCACGATACAGAGAACTTAAGCGC 562
Db 81 IleAlaProGluSerAspValAsnThrAsnTrpSerMetGluTyrAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAA 583
Db 101 LysIleGluLeuLeuGluArg 107

RESULT 5

S27109

MADS box protein AP1 - Arabidopsis thaliana

N/Alternate names: Floral homeotic protein AP1

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999

C/Accession: S27109; S36597

R/Mandel, M.A.; Gustafson-Brown, C.; Savidge, B.; Yanofsky, M.F.

Nature 360, 273-277, 1992

A/Title: Molecular characterization of the Arabidopsis floral homeotic gene AP1.

A/Reference number: S27109; MUID:93063372; PMID:1359429

A/Accession: S27109

A/Molecule type: mRNA

A/Residues: 1-256 <MAN>

A/Cross-references: EMBL:Z16421; NID:g16161; PIDN:CAA78909.1; PID:g16162

Note: 27-Asp was also found

Yanofsky, M.F.

Submitted to the EMBL Data Library, October 1992

A/Reference number: S36597

A/Accession: S36597

A/Molecule type: mRNA

A/Residues: 1-235, 237-256 <YAN>

A/Cross-references: EMBL:Z16421; NID:g16161; PIDN:CAA78909.1; PID:g16162

C/Genetics:

A/Map position: 1

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homol

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 2.31e-30 Length: 256
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x S27109 (1-256)

QY 263 ATGGGTCCGGCGCAAGTGCAGCTGAGGAGATAGAGAACAGATTAATCGCAGGTGACC 322

Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGGCGCCGCAAGCGGCTCCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgGlyArgValGlnLeuLysLysIleGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGGTCCGCGTATGCTCTTCTCCCGCAAGGCAAGCTCTATGATGACGCCACGAC 442
Db 41 AlaGluValAlaLeuValPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAACGTATGAGCGCTCTTATGCTGAAGAGGCTCTT 502
Db 61 SerCysMetGluLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGTGAAGGAAATTGGTCCACGATACAGAGAACTTAAGCGC 562
Db 81 IleAlaProGluSerAspValAsnThrAsnTrpSerMetGluTyrAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAA 583
Db 101 LysIleGluLeuLeuGluArg 107

RESULT 6

T07902

MADS box protein - Commerson's wild potato

C/Species: Solanum commersonii (Commerson's wild potato)

C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999

C/Accession: T07902

R/Seppanen, M.M.

Submitted to the EMBL Data Library, May 1997

A/Description: Nucleotide sequence of novel wild potato (Solanum commersonii) MADS-box

A/Reference number: Z16201

A/Accession: T07902

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-250 <SEP>

A/Cross-references: EMBL:AF002666; NID:g2290777; PIDN:AAB65161.1; PID:g2290778

C/Genetics:

A/Gene: SCML

C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo

C/Keywords: DNA binding; nucleus; transcription regulation

F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 4.27e-29 Length: 250
Score: 410.00 Matches: 79
Percent Similarity: 85.45% Conservative: 15
Best Local Similarity: 71.82% Mismatches: 16
Query Match: 39.81% Indels: 0
DB: 2 Gaps: 0

US-10-020-338-8 (1-593) x T07902 (1-250)

QY 263 ATGGGTCCGGCGCAAGTGCAGCTGAGGAGATAGAGAACAGATTAATCGCAGGTGACC 322
Db 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGGCGCCGCAAGCGGCTCCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
Db 21 PheSerLysArgGlyArgValGlnLeuLysLysIleGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGGTCCGCGTATGCTCTTCTCCCGCAAGGCAAGCTCTATGATGACGCCACGAC 442
Db 41 AlaGluValAlaLeuValPheSerHisLysGlyLysLeuPheGluLysSerThrAsp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAACGTATGAGCGCTCTTATGCTGAAGAGGCTCTT 502
Db 61 SerCysMetGluLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAGAGTGAAGGAAATTGGTCCACGATACAGAGAACTTAAGCGC 562
Db 81 ValProThrAspHisThrSerProGluLysSerTrpThrLeuGluAsnAlaLysLeuLysAla 100

OY 383 GCGAGGTGCGGCTGATGCTTCTCCCAAGGCAAGCTTATGATGACCCAGCCAGC 442
|||||
Db 41 AlagluvalalavalalllevalpheneserprolysglylsuylrglylralthrAsp 60
|||||
OY 443 TCCAGCATGGAACAATTTCTGAACGTTATGAGCGCTACTCTTGTGCGAAAGGCTCTT 502
|||||
Db 61 SeratrgmetasphylsileleugluarglyrgluarglyrseryrAlaagluvalaleu 80
|||||
OY 503 ATTTCAGCTGAATCTGAAGAGGAAATTTGTCGCCAGATACAGGAACTTAAAGCG 562
|||||
Db 81 lleserlagaugsergluglYasntrpCyshlsiglyrarglylsuylsAla 100
|||||
OY 563 AAGATTGAGACCATCAAAAATGTCACAAG 592
|||||
Db 101 LysileglunrllleglulysCyshlslys 110
|||||
RESULT 2
T14737
MADS box protein - sorghum (fragment)
Species: Sorghum bicolor (sorghum)
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C/Accession: T14737
R/Greco, R.; Stagli, L.; Colombo, L.; Angenent, G.C.; Sari-Gorla, M.; Pe, M.E.
Mol. Gen. Genet. 253, 615-623, 1997
A/Title: MADS box genes expressed in developing inflorescences of rice and sorghum.
A/Reference number: Z15292; MUID:97218034; PMID:9065695
A/Accession: T14737
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-228 <GRE>
A/Cross-references: EMBL:U32110; NID:G1905933; PIDN:AAB50181.1; PID:G1905934
C/Genetics:
A/Gene: MADS2
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
C/Keywords: DNA binding; nucleus; transcription regulation
Alignment Scores:
Pred. No.: 8 53e-41 Length: 228
Score: 539.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 52.33% Indels: 0
Gaps: 0
US-10-020-338-8 (1-593) x T14737 (1-228)

N/Alternate names: transcription factor, squa
C/Species: Antirrhinum majus (garden snapdragon)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Sep-1999
C/Accession: S20886
R/Hilfser, P.; Klein, J.; Loening, W.E.; Meijer, H.; Saedler, H.; Sommer, H.
EMBO J. 11, 1239-1249, 1992
A/Title: Bracteomania, an inflorescence anomaly, is caused by the loss of function of t
A/Reference number: S20886; MUID:92224862; PMID:1563342
A/Accession: S20886
A/Molecule type: DNA
A/Residues: 1-248 <HUI>
A/Cross-references: EMBL:X63701; NID:G16051; PIDN:CAA45228.1; PID:G16052
C/Genetics:
A/Gene: squa
A/Introns: 62/2; 88/3; 110/2; 143/3; 157/3; 171/3; 215/2
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
C/Keywords: DNA binding; nucleus; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>
Alignment Scores:
Pred. No.: 3.51e-31 Length: 248
Score: 433.00 Matches: 83
Percent Similarity: 88.18% Conservative: 14
Best Local Similarity: 75.45% Mismatches: 13
Query Match: 42.04% Indels: 0
Gaps: 0
US-10-020-338-8 (1-593) x S20886 (1-248)

OY 263 ATGGGTGCGGCAAGGTGACGATGAGCAAGATTAATTCGAGGTGACC 322
|||||
Db 1 MetcylargglylsvalglulnleulysargllleglulnlsylleasnaaglnvalThr 20
|||||
OY 323 TTCTCCAGCGCGCGCAACGCGCTCTGGAAGGCGCAGAGATCTCGTCTGTGAC 382
|||||
Db 21 PheSerlysarlgarglglylLeulnleulysAlaHlsiglulnserValleuCyAsp 40
|||||
OY 383 GCGAGGTGCGGCTGATGCTTCTCCCAAGGCAAGCTTATGATGACCCAGCCAGC 442
|||||
Db 41 AlagluvalalaleuilevalphenesasnlsylylsuylpneuglyrserThrAsp 60
|||||
OY 443 TCCAGCATGGAACAATTTCTGAACGTTATGAGCGCTACTCTTATGCTGAAGGCTCTT 502
|||||
Db 61 SerCysmetaspharglleleugluarglyrgluarglyrseryrAlaagluvalaleu 80
|||||
OY 503 ATTTCAGCTGAATCTGAAGAGGAAATTTGTCGCCAGATACAGGAACTTAAAGCG 562
|||||
Db 81 ValSerasngluproglnserProAlaAsntrpThrleuglulnyserylsuylsAla 100
|||||
OY 563 AAGATTGAGACCATCAAAAATGTCACAAG 592
|||||
Db 101 ArgilleglulnleuglnArgasnHlsArg 110
|||||
RESULT 4
S52236
MADS box protein ap1 - white mustard
N/Alternate names: floral homeotic protein ap1
C/Species: Sinapis alba (white mustard)
C/Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999
C/Accession: S52236
R/Menzel, G.; Apel, K.; Meizer, S.
submitted to the EMBL Data Library, September 1994
A/Description: Isolation and sequencing of the mustard (Sinapis alba L.) ap1 cDNA.
A/Reference number: S52236
A/Accession: S52236
A/Molecule type: mRNA
A/Residues: 1-254 <MEN>
A/Cross-references: EMBL:X81480; NID:G609252; PIDN:CAA57233.1; PID:G609253
C/Superfamily: transcription factor squa; serum response factor DNA-binding domain homo
C/Keywords: DNA binding; nucleus; transcription regulation
F/2-57/Domain: serum response factor DNA-binding domain homology <SRF>
Alignment Scores:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 24, 2003, 14:06:08 ; Search time 24 Seconds
(without alignments)
4750.643 Million cell updates/sec

Title: US-10-020-338-8

Perfect score: 1030
Sequence: 1 cccgctgcaccagcgtccg.....catacaaaatgtcacagc 593

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Xgapext 0.5
Xgapop 6.0 , Xgapext 7.0
Delop 6.0 , Delext 7.0

Archived: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-O=/cgn2/1/USPTO.spool/US10020338/runat_24062003_102355_21519/app_query.fasta.1.775
-DB=PIR_73 -QFMT=fasten -SUFFIX=rpt -MINMATCH=0.1 -IOOPEL=0 -IOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MYLEN=0 -MAXLEN=200000000
-USER=US10020338 @CGN 1 1 62 @runat_24062003_102355_21519 -NCPU=6 -ICPU=3
-NO MMAP -LARGEIOFURY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARK TIMEOUT=30 -THRAIDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	561	54.5	273	2 T03410
2	539	52.3	228	2 T14737
3	433	42.0	248	2 S20886
4	424	41.2	254	2 S52236
5	424	41.2	256	2 S27109
6	410	39.8	250	2 T07902
7	408	39.6	227	2 S23730
8	406	39.4	250	2 T07100
9	399	38.7	242	2 S71208
10	386	37.5	150	2 T14457
11	382	37.1	251	2 T14456
12	353.5	34.3	233	2 T10714
13	352.5	34.2	261	2 S51935
14	352.5	34.2	261	2 T09603

15	345	33.5	249	2 T04307	M79 protein - rice
16	342	33.2	249	2 T04335	MADS box protein -
17	340	33.0	248	2 T04170	MADS box protein -
18	340	33.0	259	2 T04169	MADS box protein -
19	333	32.3	231	2 T14801	MADS box protein M
20	330.5	32.1	224	2 T01690	MADS box protein f
21	330	32.0	250	2 T04167	MADS box protein -
22	329	31.9	242	2 T10486	MADS box protein -
23	329	31.9	242	2 T09571	MADS box protein M
24	327.5	31.8	245	2 T09569	MADS box protein M
25	327	31.7	247	2 S78015	MADS box protein D
26	326.5	31.7	247	2 T06543	MADS box protein D
27	325	31.6	246	2 T17023	MADS box protein I
28	322.5	31.3	255	2 T03408	MADS box protein -
29	322	31.3	248	2 B39534	MADS box protein A
30	322	31.3	250	2 D39534	MADS box protein A
31	322	31.3	262	2 T51409	MADS box protein A
32	321	31.2	243	2 S71756	MADS box protein D
33	319.5	31.0	224	2 S23728	MADS box protein T
34	318	30.9	255	2 T03398	MADS box protein -
35	317.5	30.8	242	2 S71757	MADS box protein D
36	315.5	30.6	254	2 T10467	MADS box protein D
37	314.5	30.5	251	2 T00656	MADS box protein A
38	313.5	30.4	225	2 T04168	MADS box protein A
39	308.5	30.0	250	2 S40405	MADS box protein -
40	307.5	29.9	257	2 S53306	MADS box protein M
41	305	29.6	252	2 F39534	floral homeotic pr
42	301.5	29.3	234	2 A84515	probable MADS-box
43	301.5	29.3	234	2 T52100	MADS-box transcrip
44	300	29.1	258	2 S57793	MADS box protein A
45	282	27.4	60	2 S55938	MADS box protein Z

ALIGNMENTS

RESULT 1
T03410
MADS box protein - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Sep-1999
C:Accession: T03410
R:Mena, W.; Mandel, M.A.; Lerner, D.R.; Yanofsky, M.F.; Schmidt, R.J.
Plant J. 8, 845-854, 1995
A:Title: A characterization of the MADS-box gene family in maize.
A:Reference number: Z14928; MUID:96132144; PMID:8580958
A:Accession: T03410
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-273 <MEN>
A:Cross-references: EMBL:L46400; NID:9939784; PIDN:AAB00081.1; PID:9939785
C:Genetics:
A:Note: ZAP1
C:Superfamily: transcription factor sqwa; serum response factor DNA-binding domain homo
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Alignment Scores:

Pred. No.: 8.9e-43
Score: 561.00
Percent Similarity: 99.09%
Best Local Similarity: 99.09%
Query Match: 54.47%
DB: 2
Gaps: 0

US-10-020-338-8 (1-593) x T03410 (1-273)

Oy	263	ATGGGTGCGCGCAAGGTGACGCTGACGATAGACAAGATTAATCGGACGTGAC	322
Db	1	Mctcllyarvgilyvalglnleulyarvileglnleulystleaaarvglnvalthr	20
Oy	323	TTTCTCAAGGCGCGCAACGGGCTCTCTGAAGAAGCGGACGAGATCTCCCTGTGAC	382
Db	21	PheserlysarvargaengilyleuleulystlahtsigtuleSerValleucysasp	40

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Score: 386.00 Matches: 75
Percent Similarity: 87.62% Conservative: 17
Best Local Similarity: 72.43% Mismatches: 11
Query Match: 37.48% Indels: 2
Gaps: 1

US-10-020-338-8 (1-593) x US-09-853-450-14 (1-150)

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OY 263 ATGGGTCCGGCGAGGTGCACTGTAAGCGGATAGAGACAGATAATCGGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGluMetLysArgIleGluAsnLysIleAsnArgIleValThr 20
OY 323 TTCTCCAAAGCGCGCAAGCGGCTCCGGAAGCGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgValGluLeuLysLysAlaHisGluIleSerLysLeuCySer 40
OY 383 GCGAGGTCCGCGTCACTGCTCTTCCCCCAAGGCAAGCTCATGATGACGCAACGAC 442
DB 41 AlaGluValSerLeuIleValPheSerHisLysGlyLysLeuPheGluIlyrSerArgIle 60
OY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGACCGCTACTTATCTGAAAGGCTCTT 502
DB 61 SerCyMetGluLysValLeuGluArgIlyrGluArgIlyrSerIyAlaGluLysGluLeu 80
OY 503 ATTTCAGCTGAATCT-----GAAAGTGAGGAAATTGATGCCAGATACAGAAACTT 556
DB 81 LysAlaProAspSerHisValAsnAlaGlnThrAsnTrpSerMetGluIlyrSerArgIle 100
OY 557 AAGCGAAGATTGAG 571
DB 101 LysAlaLysIleGlu 105
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RESULT 12

US-09-853-450-12
Sequence 12, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12

LENGTH: 251

TYPE: PRF
ORGANISM: Brassica oleracea
FEATURE:
OTHER INFORMATION: CAULIFLOWER (CAL)

US-09-853-450-12

Alignment Scores:
Pred. No.: 8.6e-29 Length: 251
Score: 382.00 Matches: 74
Percent Similarity: 85.32% Conservative: 19
Best Local Similarity: 67.89% Mismatches: 14
Query Match: 37.09% Indels: 2
Gaps: 1

US-10-020-338-8 (1-593) x US-09-853-450-12 (1-251)

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OY 263 ATGGGTCCGGCGAGGTGCACTGTAAGCGGATAGAGACAGATAATCGGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGluMetLysArgIleGluAsnLysIleAsnArgIleValThr 20
OY 323 TTCTCCAAAGCGCGCAAGCGGCTCCGGAAGCGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgValGluLeuLysLysAlaHisGluIleSerLysLeuCySer 40
```

```
OY 383 GCGAGGTCCGCGTCACTGCTTCTCCCCCAAGGCAAGCTCTATGATGACGCAACGAC 442
DB 41 AlaGluValSerLeuIleValPheSerHisLysGlyLysLeuPheGluIlyrSerArgIle 60
OY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGACCGCTACTTATGCTGAAAGGCTCTT 502
DB 61 SerCyMetGluLysValLeuGluArgIlyrGluArgIlyrSerIyAlaGluLysGluLeu 80
OY 503 ATTTCAGCTGAATCT-----GAAAGTGAGGAAATTGCTGCCAGATACAGAAACTT 556
DB 81 LysValProAspSerHisValAsnAlaGlnThrAsnTrpSerValGluIlyrSerArgIle 100
OY 557 AAGCGAAGATTGAGACCATCAAAA 583
DB 101 LysAlaLysIleGluLeuGluArg 109
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RESULT 13

US-09-853-450-28
Sequence 28, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 248
TYPE: PRF
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: SEPALLATA1 (SEPI)

US-09-853-450-28

Alignment Scores:
Pred. No.: 5.94e-23 Length: 248
Score: 322.00 Matches: 63
Percent Similarity: 78.50% Conservative: 21
Best Local Similarity: 58.88% Mismatches: 23
Query Match: 31.26% Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-09-853-450-28 (1-248)

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OY 263 ATGGGTCCGGCGAGGTGCACTGTAAGCGGATAGAGACAGATAATCGGCGAGTACC 322
DB 1 MetGlyArgGlyArgValGluMetLysArgIleGluAsnLysIleAsnArgIleValThr 20
OY 323 TTCTCCAAAGCGCGCAAGCGGCTCTTGAAGCGCGCAGATCTCCGCTCTGTGAC 382
DB 21 PheAlaLysArgArgValGluLeuLysLysAlaIlyrGluLeuSerValLeuCySer 40
OY 383 GCGAGGTCCGCGTCACTGCTTCTCCCCCAAGGCAAGCTCATGATGACGCAACGAC 442
DB 41 AlaGluValAlaLeuIleIlePheSerAsnArgIlyrLysLeuIlyrGluPheCySerSer 60
OY 443 TCCAGCATGACAAATTTCTTGAAGCTTATGAGCGCTACTTATGCTGAAAGGCTCTT 502
DB 61 SerAsnMetLeuIlyrThrLeuAspArgIlyrGluLysCySerIyGlySerIleGluVal 80
OY 503 ATTTCAGCTGAATCTGAAAGTAGGAAATTGCTGCCAGATACAGAAACTTAAAGCG 562
DB 81 AsnAsnLysProAlaLysGluLeuGluLysSerIyArgGluIlyrLeuLysLeuLysGly 100
OY 563 AAGATTGAGACCATCAAAA 583
DB 101 LysAlaLysIleGluLeuGluArg 109
```

```

Db      101 ArgValGluValLeuGluIuIys 107
      :::::||||| :::::|||||
RESULT 9
US-09-978-730-2
Sequence 2, Application US/09978730
Patent No. US20020129403A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Liljegen, Sarah
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
FILE REFERENCE: 19452A-000920US
CURRENT APPLICATION NUMBER: US/09/978,730
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-978-730-2

Alignment Scores:
Pred. No.: 1,898-30 Length: 242
Score: 399.00 Matches: 75
Percent Similarity: 85.98% Conservative: 17
Best Local Similarity: 70.09% Mismatches: 15
Query Match: 38.74% Indels: 0
DB: 10 Gaps: 0
US-10-020-338-8 (1-593) x US-09-978-730-2 (1-242)
QY 263 ATGGGTGCGCGGCAAGGTGCACTGAAGCGGATAGAAACAAGTAAATGCGCAGGTGACC 3222
Db 1 MetGlyArgGlyValGlyAlaGlnLeuLysArgGlyLeuGlnValLeuThr 20
QY 323 TTCTCCAAAGCGCGGCAAGCGGCTCTCTGAAGAAAGCGGACAGATTTCCGTCTCTGTGAC 3822
Db 21 PheSerLysArgArgSerGlyLeuLysLysAlaHisGlnIleSerValLeuGlnCysAsp 40
QY 383 GCGGAGGTGCGCGTCAATCGCTCTTCTCCGCCCAAGGCAAGCTGTATAGTACGACCGAC 4422
Db 41 AlGluValAlaLeuIleValPheSerSerLysGlyLysLeuPheGluIuIysSerThrAsp 60
QY 443 TCCAGCATGACAAAAATCTTGAACCTTATGAGCGCTACTCTTATGCTGAAGAAAGCTCTT 5022
Db 61 SerCysMetClnArgIleLeuGlnArgGlyIraAspArgGlyLeuIuIysSerAspLysGlnLeu 80
QY 503 ATTTCACCTGAATCTGAAGAGGAGAAATTGGTGCACGAATACAGGAAACTTAAGCGC 5622
Db 81 ValGlyArgAspArgLysSerGlnSerGlnIleValLeuGlnIuIleValLysLeuLysAla 1000
QY 563 AAGATTGAGCCATACAAAAA 583
Db 101 ArgValGluValLeuGluIuIys 107
      :::::||||| :::::|||||
RESULT 10
US-09-853-450-10
Sequence 10, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development

```

```

FILE REFERENCE : 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 255
TYPE: PRF
ORGANISM: Arabidopsis thaliana
FEATURE:
/ OTHER INFORMATION: CAULIFLOWER (CAL)
US-09-853-450-10.

Alignment Scores:
Pred. No.:          9,18e-30          Length:          255
Score:              392.00            Matches:          76
Percent Similarity: 87.16%            Conservative:    19
Best Local Similarity: 69.72%          Mismatches:     12
Query Match:        38.06%            Indels:         2
DB:                  9                Gaps:            1

US-10-020-338-8 (1-593) x US-09-853-450-10 (1-255)

QY      263  ATGGATCGCGGCGAGGTGCAGCTGAGGCGGATAGGAACAAGATAATCGCAGGTGACC 322
Db      1  MGGIYARGIYARGIYALGluuYsArgIleGluuSnlYsIleAaHAGInValThr 20
        |||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY      323  TTCTCCAAAGCGCGGCAACGGGCTCTCTGAAGAGGCGCAGAGATCTCCGTCTGTGAC 382
Db      21  PheSerIyARgARgthrgIyLeuSnlYsIySAlaGInGInIleSerValLeuCYaSp 40
        |||:::||||:||||:||||:||||:||||:||||:||||:||||:
QY      383  GCGGAGGTGCGCGTCATGCTCTTCTCCCCCAAAGCGCAAGCTCTATGAGTACGCCAGC 442
Db      41  AlaGluValSerIleuLeValPheSerHIsYsGlySLeuPheGluYrSerSerGlu 60
        |||:::||||:||||:||||:||||:||||:||||:||||:||||:
QY      443  TTCAGATGAGCAAAATTTGTAAGCTATGAGCGCTACTTATGCTGAAAAGGCTCTT 502
Db      61  SerCYmeGluYsValleuGInuArgYrGluuArgYrSerYrAlaGluArgInleu 80
        |||:::||||:||||:||||:||||:||||:||||:||||:||||:
QY      503  ATTTCAGCTGAATCT-----GAAAGTGAAGGAAATTGGTGCCACGAATACAGGAACTT 556
Db      81  IleAlaProAspSerHisValAsnAlaGInThrAsnTrpSerMetGluYrSerArgleu 100
        |||:::||||:||||:||||:||||:||||:||||:||||:||||:
QY      557  AAGCGAAGATTGAGACCTATACAAAA 583
Db      101  LysAlaLysIleGluLeuDeuGluArg 109
        |||:::||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
US-09-853-450-14
/ Sequence 14, Application US/09853450
/ Publication No. US20020194645A1
/ GENERAL INFORMATION:
/ APPLICANT: Yanofsky, Martin F.
/ APPLICANT: Pelaz, Soraya
/ APPLICANT: Ditta, Gary
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
/ FILE REFERENCE: 19452A-002400US
/ CURRENT APPLICATION NUMBER: US/09/853,450
/ CURRENT FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
LENGTH: 150
TYPE: PRF
ORGANISM: Brassica oleracea var. botrytis
FEATURE:
/ OTHER INFORMATION: CAULIFLOWER (CAL)
US-09-853-450-14

Alignment Scores:
Pred. No.:          3.08e-29          Length:          150

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Percent Similarity: 85.98% Conservative: 17
Best Local Similarity: 70.09% Mismatches: 15
Query Match: 38.74% Indels: 0
DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-981-087A-2 (1-242)

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QY 263 ATGGTCGGCGGCGAGCTGACGTGAAGCGGATGAGAACAGATTAATCGCGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysAlaHisLeuSerValThr 20
QY 323 TTCTCCAGCGCGCGAGCTCTCCGAGAGAGCGCAGCATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGGTGCGCGTCATCTCTTCTCCCAAGAGCGCAGCTCTATGATGACCGAC 442
DB 41 AlaGluValAlaLeuIleValPheSerSerLysGlyLeuPheGlnLysSerThrAsp 60
QY 443 TCACGATGACAAATTTTGAACGTTATGACGCTACTCTTATGCTGAAAAGCTCTT 502
DB 61 SerCysMetGluArgIleLeuGlnLysArgIleLysArgIleLysSerAspLysGlnLeu 80
QY 503 ATTTGACGTAATCTGAAAGTGAAGTGAAGGAAATTGGTCCAGAAATPACAGAACTTAAGCGC 562
DB 81 ValGlyArgAspValSerGlnSerGlnSerGlnSerValLeuGlnHisAlaLysLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAAA 583
DB 101 ArgValGluValLeuGlnLys 107
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RESULT 7

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US-09-978-382A-2
; Sequence 2, Application US/0978382A
; Publication No. US20020194647A1
; GENERAL INFORMATION:
; APPLICANT: YanoFsky, Martin F.
; APPLICANT: Liljgren, Sarah
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000930US
; CURRENT APPLICATION NUMBER: US/09/978,382A
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-382A-2
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Alignment Scores:

Pred. No.:	1,89e-30	Length:	242
Score:	399.00	Matches:	75
Percent Similarity:	85.98%	Conservative:	17
Best Local Similarity:	70.09%	Mismatches:	15
Query Match:	38.74%	Indels:	0
DB:	9	Gaps:	0

US-10-020-338-8 (1-593) x US-09-978-382A-2 (1-242)

```
QY 263 ATGGTCGGCGGCGAGCTGACGTGAAGCGGATGAGAACAGATTAATCGCGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysAlaHisLeuSerValThr 20
QY 323 TTCTCCAGCGCGCGAGCTCTCCGAGAGAGCGCAGCATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
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```
QY 383 GCGGAGGTGCGCGTCATCTCTTCTCCCAAGAGCGCAGCTCTATGATGACCGAC 442
DB 41 AlaGluValAlaLeuIleValPheSerSerLysGlyLeuPheGlnLysSerThrAsp 60
QY 443 TCACGATGACAAATTTTGAACGTTATGACGCTACTCTTATGCTGAAAAGCTCTT 502
DB 61 SerCysMetGluArgIleLeuGlnLysArgIleLysArgIleLysSerAspLysGlnLeu 80
QY 503 ATTTGACGTAATCTGAAAGTGAAGTGAAGGAAATTGGTCCAGAAATPACAGAACTTAAGCGC 562
DB 81 ValGlyArgAspValSerGlnSerGlnSerGlnSerValLeuGlnHisAlaLysLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAAA 583
DB 101 ArgValGluValLeuGlnLys 107
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RESULT 8

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US-09-978-740A-2
; Sequence 2, Application US/0978740A
; Publication No. US2003005481A1
; GENERAL INFORMATION:
; APPLICANT: YanoFsky, Martin F.
; APPLICANT: Liljgren, Sarah
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
; FILE REFERENCE: 19452A-000960US
; CURRENT APPLICATION NUMBER: US/09/978,740A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: US 60/090,649
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: US 09/339,998
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-978-740A-2
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Alignment Scores:

Pred. No.:	1,89e-30	Length:	242
Score:	399.00	Matches:	75
Percent Similarity:	85.98%	Conservative:	17
Best Local Similarity:	70.09%	Mismatches:	15
Query Match:	38.74%	Indels:	0
DB:	9	Gaps:	0

US-10-020-338-8 (1-593) x US-09-978-740A-2 (1-242)

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QY 263 ATGGTCGGCGGCGAGCTGACGTGAAGCGGATGAGAACAGATTAATCGCGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGlnLysAlaHisLeuSerValThr 20
QY 323 TTCTCCAGCGCGCGAGCTCTCCGAGAGAGCGCAGCATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGGAGGTGCGCGTCATCTCTTCTCCCAAGAGCGCAGCTCTATGATGACCGAC 442
DB 41 AlaGluValAlaLeuIleValPheSerSerLysGlyLeuPheGlnLysSerThrAsp 60
QY 443 TCACGATGACAAATTTTGAACGTTATGACGCTACTCTTATGCTGAAAAGCTCTT 502
DB 61 SerCysMetGluArgIleLeuGlnLysArgIleLysArgIleLysSerAspLysGlnLeu 80
QY 503 ATTTGACGTAATCTGAAAGTGAAGTGAAGGAAATTGGTCCAGAAATPACAGAACTTAAGCGC 562
DB 81 ValGlyArgAspValSerGlnSerGlnSerGlnSerValLeuGlnHisAlaLysLeuLysAla 100
QY 563 AAGATTGAGACCATACAAAAA 583
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RESULT 4
US-09-853-450-6
; Sequence 6, Application US/09853450
; Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Datta, Gary
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
FILE REFERENCE: 19452A-002400US
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 255
; TYPE: prt
; ORGANISM: Brassica oleracea var. botrytis
FEATURE:
OTHER INFORMATION: APETALAI (AP1)
US-09-853-450-6

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Best Local Similarity: 99.09% Mismatches: 1
Query Match: 54.47% Indels: 0
DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-853-450-8 (1-273)

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QY 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAGAGCGCCAGAGATCTCCGCTCTGTGAC 382
|||
DB 21 PheSerLysArgArgSerGlnLeuLysLysAlaHisGlnIleSerValLeuCyAsp 40
QY 383 GCGAGGTGCGGCTGATGCTTCTTCCCGCAAGGCAAGCTTATGATGACCGAC 442
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DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuLysGlnIleValThrAsp 60
QY 443 TCCAGCATGACAAATTTCTGAAGCTTATGAGCGGCTCTTATGCTGAAGAGGCTTT 502
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DB 61 SerArgMetAspLysIleLeuGlnArgIleGlnLysSerIleValGlnLysAlaLeu 80
QY 503 ATTTGAGTGAATCTGAAGAGTGAAGGAAATGGTGCACGAATACAGAACTTAAGCG 562
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DB 81 IleSerAlaGlnSerGlnSerGlnLysGlnValThrPheGlnIleValArgLysLeuLysAla 100
QY 563 AAGATTGAGACCATACAAATAATGTCAAG 592
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DB 101 LysIleGlnLysIleGlnLysCysHisLys 110

RESULT 2

US-09-853-450-4
/ Sequence 4, Application US/09853450
/ Publication No. US20020194645A1
/ GENERAL INFORMATION:
/ APPLICANT: Vanofsky, Martin F.
/ APPLICANT: Pelaz, Soraya
/ APPLICANT: Ditle, Gary
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
/ FILE REFERENCE: 19452A-002400US
/ CURRENT APPLICATION NUMBER: US/09/853,450
/ CURRENT FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 253
/ TYPE: PRT
/ ORGANISM: Brassica oleracea
/ FEATURE:
/ OTHER INFORMATION: APETALAI (AP1)

US-09-853-450-4

Alignment Scores:
Pred. No.: 2,87e-33 Length: 253
Score: 428.00 Matches: 82
Percent Similarity: 89.72% Conservative: 14
Best Local Similarity: 76.64% Mismatches: 11
Query Match: 41.55% Indels: 0
DB: 9 Gaps: 0

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QY 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAGAGCGCCAGAGATCTCCGCTCTGTGAC 382
|||
DB 21 PheSerLysArgArgSerGlnLeuLysLysAlaHisGlnIleSerValLeuCyAsp 40
QY 383 GCGAGGTGCGGCTGATGCTTCTTCCCGCAAGGCAAGCTTATGATGACCGAC 442

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DB 41 AlaGlnValAlaValIleValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGACAAATTTCTGAAGCTTATGAGCGGCTCTTATGCTGAAGAGGCTTT 502
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DB 61 SerCysMetGlnLysIleLeuGlnLysArgIleGlnLysSerIleValGlnLysAlaLeu 80
QY 503 ATTTGAGTGAATCTGAAGAGTGAAGGAAATGGTGCACGAATACAGAACTTAAGCG 562
|||
DB 81 IleAlaProGlnSerAspSerAsnThrAsnThrSerMetGlnLysAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAATAATGTCAAG 592
|||
DB 101 LysIleGlnLysLeuGlnLysArg 107

RESULT 3

US-09-853-450-2
/ Sequence 2, Application US/09853450
/ Publication No. US20020194645A1
/ GENERAL INFORMATION:
/ APPLICANT: Vanofsky, Martin F.
/ APPLICANT: Pelaz, Soraya
/ APPLICANT: Ditle, Gary
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
/ FILE REFERENCE: 19452A-002400US
/ CURRENT APPLICATION NUMBER: US/09/853,450
/ CURRENT FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 256
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ OTHER INFORMATION: APETALAI (AP1)

US-09-853-450-2

Alignment Scores:
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Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: 9 Gaps: 0

US-10-020-338-8 (1-593) x US-09-853-450-2 (1-256)

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DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAGAGCGCCAGAGATCTCCGCTCTGTGAC 382
|||
DB 21 PheSerLysArgArgSerGlnLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGAGGTGCGGCTGATGCTTCTTCCCGCAAGGCAAGCTTATGATGACCGAC 442
|||
DB 41 AlaGlnValAlaValIleValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGACAAATTTCTGAAGCTTATGAGCGGCTCTTATGCTGAAGAGGCTTT 502
|||
DB 61 SerCysMetGlnLysIleLeuGlnLysArgIleGlnLysSerIleValGlnLysAlaLeu 80
QY 503 ATTTGAGTGAATCTGAAGAGTGAAGGAAATGGTGCACGAATACAGAACTTAAGCG 562
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DB 81 IleAlaProGlnSerAspSerAsnThrAsnThrSerMetGlnLysAsnArgLeuLysAla 100
QY 563 AAGATTGAGACCATACAAATAATGTCAAG 583
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DB 101 LysIleGlnLysLeuGlnLysArg 107

GenCore version 5.1.6
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Run on: June 24, 2003, 14:09:43 ; Search time 28.5 Seconds

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Title: US-10-020-338-8

Perfect score: 1030

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Minimum DB seq length: 0

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Maximum Match 100%
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Database : Published Applications_AA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	428	41.6	253	US-09-853-450-4
3	424	41.2	256	US-09-853-450-2
4	422	41.0	255	US-09-853-450-6

5	399	38.7	242	9	US-09-978-729A-2	Sequence 2, Appli
6	399 <th>38.7</th> <th>242</th> <th>9</th> <th>US-09-981-087A-2</th> <th>Sequence 2, Appli</th>	38.7	242	9	US-09-981-087A-2	Sequence 2, Appli
7	399 <th>38.7</th> <th>242</th> <th>9</th> <th>US-09-978-382A-2</th> <th>Sequence 2, Appli</th>	38.7	242	9	US-09-978-382A-2	Sequence 2, Appli
8	399 <th>38.7</th> <th>242</th> <th>9</th> <th>US-09-978-740A-2</th> <th>Sequence 2, Appli</th>	38.7	242	9	US-09-978-740A-2	Sequence 2, Appli
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10	399 <th>38.7</th> <th>242</th> <th>10</th> <th>US-09-978-730-2</th> <th>Sequence 2, Appli</th>	38.7	242	10	US-09-978-730-2	Sequence 2, Appli
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12	382 <th>37.1</th> <th>251</th> <th>9</th> <th>US-09-853-450-12</th> <th>Sequence 12, Appli</th>	37.1	251	9	US-09-853-450-12	Sequence 12, Appli
13	382 <th>37.1</th> <th>248</th> <th>9</th> <th>US-09-853-450-12</th> <th>Sequence 14, Appli</th>	37.1	248	9	US-09-853-450-12	Sequence 14, Appli
14	332 <th>31.3</th> <th>250</th> <th>9</th> <th>US-09-853-450-28</th> <th>Sequence 28, Appli</th>	31.3	250	9	US-09-853-450-28	Sequence 28, Appli
15	314.5 <th>29.3</th> <th>237</th> <th>9</th> <th>US-09-853-450-30</th> <th>Sequence 30, Appli</th>	29.3	237	9	US-09-853-450-30	Sequence 30, Appli
16	301.5 <th>29.3</th> <th>234</th> <th>9</th> <th>US-09-853-450-32</th> <th>Sequence 32, Appli</th>	29.3	234	9	US-09-853-450-32	Sequence 32, Appli
17	276.5 <th>26.8</th> <th>214</th> <th>9</th> <th>US-09-819-142-16</th> <th>Sequence 16, Appli</th>	26.8	214	9	US-09-819-142-16	Sequence 16, Appli
18	276.5 <th>26.8</th> <th>238</th> <th>9</th> <th>US-09-853-450-34</th> <th>Sequence 34, Appli</th>	26.8	238	9	US-09-853-450-34	Sequence 34, Appli
19	274.5 <th>26.7</th> <th>248</th> <th>9</th> <th>US-10-104-580-16</th> <th>Sequence 16, Appli</th>	26.7	248	9	US-10-104-580-16	Sequence 16, Appli
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23	274.5 <th>26.7</th> <th>248</th> <th>9</th> <th>US-09-978-740A-4</th> <th>Sequence 4, Appli</th>	26.7	248	9	US-09-978-740A-4	Sequence 4, Appli
24	273.5 <th>26.6</th> <th>241</th> <th>9</th> <th>US-09-978-730-6</th> <th>Sequence 4, Appli</th>	26.6	241	9	US-09-978-730-6	Sequence 4, Appli
25	269.5 <th>26.2</th> <th>246</th> <th>9</th> <th>US-10-104-580-12</th> <th>Sequence 12, Appli</th>	26.2	246	9	US-10-104-580-12	Sequence 12, Appli
26	269.5 <th>26.2</th> <th>246</th> <th>9</th> <th>US-09-978-729A-6</th> <th>Sequence 6, Appli</th>	26.2	246	9	US-09-978-729A-6	Sequence 6, Appli
27	269.5 <th>26.2</th> <th>246</th> <th>9</th> <th>US-09-981-087A-6</th> <th>Sequence 6, Appli</th>	26.2	246	9	US-09-981-087A-6	Sequence 6, Appli
28	269.5 <th>26.2</th> <th>246</th> <th>9</th> <th>US-09-978-382A-6</th> <th>Sequence 6, Appli</th>	26.2	246	9	US-09-978-382A-6	Sequence 6, Appli
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31	257 <th>25.0</th> <th>240</th> <th>9</th> <th>US-09-819-142-18</th> <th>Sequence 18, Appli</th>	25.0	240	9	US-09-819-142-18	Sequence 18, Appli
32	254 <th>24.7</th> <th>228</th> <th>9</th> <th>US-10-295-403-70</th> <th>Sequence 70, Appli</th>	24.7	228	9	US-10-295-403-70	Sequence 70, Appli
33	248 <th>24.1</th> <th>240</th> <th>10</th> <th>US-09-819-142-4</th> <th>Sequence 4, Appli</th>	24.1	240	10	US-09-819-142-4	Sequence 4, Appli
34	246.5 <th>23.9</th> <th>219</th> <th>9</th> <th>US-09-970-624-2</th> <th>Sequence 2, Appli</th>	23.9	219	9	US-09-970-624-2	Sequence 2, Appli
35	236.5 <th>23.0</th> <th>173</th> <th>9</th> <th>US-10-278-173-130</th> <th>Sequence 130, App</th>	23.0	173	9	US-10-278-173-130	Sequence 130, App
36	236 <th>22.9</th> <th>256</th> <th>9</th> <th>US-09-853-450-40</th> <th>Sequence 40, Appli</th>	22.9	256	9	US-09-853-450-40	Sequence 40, Appli
37	236 <th>22.9</th> <th>256</th> <th>9</th> <th>US-10-286-264-62</th> <th>Sequence 62, Appli</th>	22.9	256	9	US-10-286-264-62	Sequence 62, Appli
38	234 <th>22.7</th> <th>507</th> <th>10</th> <th>US-10-286-264-62</th> <th>Sequence 62, Appli</th>	22.7	507	10	US-10-286-264-62	Sequence 62, Appli
39	234 <th>22.7</th> <th>507</th> <th>10</th> <th>US-09-876-187-2</th> <th>Sequence 68, Appli</th>	22.7	507	10	US-09-876-187-2	Sequence 68, Appli
40	230 <th>22.3</th> <th>227</th> <th>9</th> <th>US-09-749-728B-13</th> <th>Sequence 2, Appli</th>	22.3	227	9	US-09-749-728B-13	Sequence 2, Appli
41	227.5 <th>22.1</th> <th>228</th> <th>9</th> <th>US-09-819-142-14</th> <th>Sequence 14, Appli</th>	22.1	228	9	US-09-819-142-14	Sequence 14, Appli
42	226.5 <th>22.0</th> <th>521</th> <th>10</th> <th>US-10-286-264-34</th> <th>Sequence 34, Appli</th>	22.0	521	10	US-10-286-264-34	Sequence 34, Appli
43	223.5 <th>21.7</th> <th>465</th> <th>10</th> <th>US-09-749-728B-19</th> <th>Sequence 19, Appli</th>	21.7	465	10	US-09-749-728B-19	Sequence 19, Appli
44	223.5 <th>21.7</th> <th>473</th> <th>10</th> <th>US-09-749-728B-17</th> <th>Sequence 17, Appli</th>	21.7	473	10	US-09-749-728B-17	Sequence 17, Appli
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ALIGNMENTS

RESULT 1
US-09-853-450-8
; Sequence 8, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
; APPLICANT: Vanoesky, Martin F.
; APPLICANT: Pelaz, Soraya
; APPLICANT: Ditta, Gary
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
; FILE REFERENCE: 19452A-002400US
; CURRENT APPLICATION NUMBER: US/09/853,450
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: APETALAI (ApI)
US-09-853-450-8
Alignment Scores:
Pred. No.: 3,31e-46 Length: 273
Score: 561:00 Matches: 109
Percent Similarity: 99.09% Conservative: 0

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APPLICANT: Yanofsky, Martin F
 TITLE OF INVENTION: Maize and Cauliflower APETAL4 Gene
 TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/655,227
 FILING DATE: 05-JUN-1996
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-UD 2143
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 256 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-655-227-2.

ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,156
FILING DATE: 12-21-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360,336
FILING DATE: 12-21-94
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07251/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-576-156-2

Alignment Scores:
Pred. No.: 1,126-37 Length: 255
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: Gaps: 0

US-10-020-338-8 (1-593) x US-08-576-156-2 (1-255)

QY 263 ATGGGTCGGCGGAGGTGAGCGGATGAGAAAGATAAATTCGGCGGTGAC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAAGCGGCTCTGTAAGAAAGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlyLeuLeuLysLysAlaHisGlnIleSerValLeuCyAsp 40
QY 383 GCGGAGTCGCCGCTCATCTCTTCTCCCCAAAGCAAGCTCTATAGTAGCGCACCGAC 442
DB 41 AlaGlnValAlaLeuValAlaPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGATGAGCAAAATTTCTTGAACGTTATGACGCTACTTATAGTAAAGGCTCTT 502
DB 61 SerCysMetGlnLysIleLeuGlnArgIleGlnArgIleSerLysArgIleGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGAAATTGTCGACCAATATACAGAACTTAAGCG 562
DB 81 IleAlaProGlnSerAspValAsnThrAsnTrpSerMetGlnLysArgLeuLysAla 100
QY 563 AAGATTGAGCACTACCAAAA 583
DB 101 LysIleGlnLeuGlnArg 107

RESULT 14
US-08-659-188-2
Sequence 2, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8849
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-188-2

Alignment Scores:
Pred. No.: 1,136-37 Length: 256
Score: 424.00 Matches: 82
Percent Similarity: 88.79% Conservative: 13
Best Local Similarity: 76.64% Mismatches: 12
Query Match: 41.17% Indels: 0
DB: Gaps: 0

US-10-020-338-8 (1-593) x US-08-659-188-2 (1-256)

QY 263 ATGGTCCGCGGCAAGTCACTGTAAGCGGATGAGAAAGATAAATTCGGCGGTGAC 322
DB 1 MetGlyArgGlyArgValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGCAAGCGGCTCTGTAAGAAAGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlyLeuLeuLysLysAlaHisGlnIleSerValLeuCyAsp 40
QY 383 GCGGAGTCGCCGCTCATCTCTTCTCCCCAAAGCAAGCTCTATAGTAGCGCACCGAC 442
DB 41 AlaGlnValAlaLeuValAlaPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGATGAGCAAAATTTCTTGAACGTTATGACGCTACTTATAGTAAAGGCTCTT 502
DB 61 SerCysMetGlnLysIleLeuGlnArgIleGlnArgIleSerLysArgIleGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAAGGAAATTGTCGACCAATATACAGAACTTAAGCG 562
DB 81 IleAlaProGlnSerAspValAsnThrAsnTrpSerMetGlnLysArgLeuLysAla 100
QY 563 AAGATTGAGCACTACCAAAA 583
DB 101 LysIleGlnLeuGlnArg 107

RESULT 15
US-08-655-227-2
Sequence 2, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-227-4

Alignment Scores:
Pred. No.: 4,146-38
Score: 428.00
Percent Similarity: 89.72%
Best Local Similarity: 76.64%
Query Match: 41.55%
DB: 3
Matches: 82
Conservative: 14
Mismatches: 11
Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-227-4 (1-253)

QY 263 ATGGGTCCGCGGCAAGTGTGAGTGAAGCGGATGAGAACAGATTAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuYsArgGlieGlnAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGGCAAGCGGCTCTGAAAGAGCGCAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlyLeuMetLysValIleGlnIleSerValLeuYsAsp 40
QY 383 GGGAGGTGCGCGTATGCTCTTCTCCCGCAAGGAGTGTATAGTACGCGACCGAC 442
DB 41 AlaGlnValAlaLeuValIlePheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAGGCTCTT 502
DB 61 SerCysMetGlnLysIleLeuGlnArgGlyArgLysSerThrIleGlnArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAGGAAATTGTGCGCAGATACAGGAACTTAAGCGG 562
DB 81 IleAlaProGlnSerAspSerAsnThrAsnTrpSerMetGlnLysAsnArgLeuYsAla 100
QY 563 AAGATTGAGACCATACAAAA 583
DB 101 LysIleGlnLeuGlnArg 107

RESULT 10
US-08-655-241-4
Sequence 4, Application US/08655241
Patent No. 6025543
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigel, Declaf
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-241-4

Alignment Scores:
Pred. No.: 4,146-38
Score: 428.00
Percent Similarity: 89.72%
Best Local Similarity: 76.64%
Query Match: 41.55%
DB: 3
Matches: 82
Conservative: 14
Mismatches: 11
Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-241-4 (1-253)

QY 263 ATGGGTCCGCGGCAAGTGTGAGTGAAGCGGATGAGAACAGATTAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyArgValGlnLeuYsArgGlieGlnAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGGCAAGCGGCTCTGAAAGAGCGCAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgIleGlyLeuMetLysValIleGlnIleSerValLeuYsAsp 40
QY 383 GGGAGGTGCGCGTATGCTCTTCTCCCGCAAGGAGTGTATAGTACGCGACCGAC 442
DB 41 AlaGlnValAlaLeuValIlePheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAGGCTCTT 502
DB 61 SerCysMetGlnLysIleLeuGlnArgGlyArgLysSerThrIleGlnArgGlnLeu 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAGGAAATTGTGCGCAGATACAGGAACTTAAGCGG 562
DB 81 IleAlaProGlnSerAspSerAsnThrAsnTrpSerMetGlnLysAsnArgLeuYsAla 100
QY 563 AAGATTGAGACCATACAAAA 583
DB 101 LysIleGlnLeuGlnArg 107

RESULT 11
US-09-149-976-4
Sequence 4, Application US/09149976
Patent No. 6127123
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
APPLICANT: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

FILED DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-214A-4

Alignment Scores:
Pred. No.: 4,146-38
Score: 428.00
Percent Similarity: 89.72%
Best Local Similarity: 76.64%
Query Match: 41.55%
DB: 2
Matches: 82
Conservative: 14
Mismatches: 11
Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-08-592-214A-4 (1-253)

QY 263 ATGGGTCGGCGGCGGCTGAAGCGGATGAGAACAGATAATCGGCGAGTGACC 322
DB 1 MetGLYARGGLYARGVALGlnLeuLYSArgLIEGlnuSNLYSLasnArgGlnValThr 20
QY 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLYSArgArgLagLYLeuMetLYSValahIEGlnuIEserValLeuCYsarp 40
QY 383 GCGAGGTGCGCGCTCATCGTCTTCCGCCAAGGCAAGCTATAGTAGCCGAC 442
DB 41 AlagluValAlaLeuValValPheSerHISLYSGLYLeuPheGlnuLYrSerThrarp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTCTTATGCTGAAGGCTTT 502
DB 61 SerCYsMetGlnuLYSILEuGlnuArgTYrGlnuArgTYrSerTYrAlagluArgGlnLeu 80
QY 503 ATTTCAGTGAATCTGAAGTGAAGGGAATTGGTGCACGAAATACAGAACTTAAGGCG 562
DB 81 IleAlaProGlnuSerAspSeranThrSerMetGlnuTYrAsnArgLeuLYSala 100
QY 563 AAGATTGAGACCATACAAA 583
DB 101 LysILEGlnuLeuGlnuArg 107

RESULT 8

US-08-659-188-4
Sequence 4, Application US/08659188
Patent No. 6002069
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/659,188
FILED DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-188-4

Alignment Scores:
Pred. No.: 4,146-38
Score: 428.00
Percent Similarity: 89.72%
Best Local Similarity: 76.64%
Query Match: 41.55%
DB: 3
Matches: 82
Conservative: 14
Mismatches: 11
Indels: 0
Gaps: 0

US-10-020-338-8 (1-593) x US-08-659-188-4 (1-253)

QY 263 ATGGGTCGGCGGCGGCTGAAGCGGATGAGAACAGATAATCGGCGAGTGACC 322
DB 1 MetGLYARGGLYARGVALGlnLeuLYSArgLIEGlnuSNLYSLasnArgGlnValThr 20
QY 323 TTCTCCAGCGCGCGCAACGGGCTCTGAAGAGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLYSArgArgLagLYLeuMetLYSValahIEGlnuIEserValLeuCYsarp 40
QY 383 GCGAGGTGCGCGCTCATCGTCTTCCGCCAAGGCAAGCTATAGTAGCCGAC 442
DB 41 AlagluValAlaLeuValValPheSerHISLYSGLYLeuPheGlnuLYrSerThrarp 60
QY 443 TCCAGCATGAGCAAAATTTCTGAAGCTTATGAGCGCTACTCTTATGCTGAAGGCTTT 502
DB 61 SerCYsMetGlnuLYSILEuGlnuArgTYrGlnuArgTYrSerTYrAlagluArgGlnLeu 80
QY 503 ATTTCAGTGAATCTGAAGTGAAGGGAATTGGTGCACGAAATACAGAACTTAAGGCG 562
DB 81 IleAlaProGlnuSerAspSeranThrSerMetGlnuTYrAsnArgLeuLYSala 100
QY 563 AAGATTGAGACCATACAAA 583
DB 101 LysILEGlnuLeuGlnuArg 107

RESULT 9

US-08-655-227-4
Sequence 4, Application US/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APERALAI Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

REFERENCE/DOCKET NUMBER: P-UD 3291

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-149-976-8

Alignment Scores:

Pred. No.:	1,736-52	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	3	Gaps:	0

US-10-020-338-8 (1-593) x US-09-149-976-8 (1-273)

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QY 263 ATGGTCGCGGCAAGTCGACGTGAAGCGGATAGAGAACAGATTAATCGGACGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuYsArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGGCAAGCGGCTCTGAAAGAGCGGCAAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgLysAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuGlyAsp 40
QY 383 GGGAGAGTCGCGGTCATCTCTTCTCCCAAGGCAAGCTCATAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuYsArgIleValThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGACCGCTACTCTTATGCTGAAAGGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAGGAAATTTGTCGACGATACGAACTTAAGGCG 562
DB 81 IleSerAlaGlnSerGlnSerGlnLysArgTyrPheGlnLysArgLysLeuYsAla 100
QY 563 AAGATTGAGACCATACAAAAATGTCACAAG 592
DB 101 LysIleGlnThrIleGlnLysCysHisLys 110
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RESULT 6

US-09-398-326-8

Sequence 8, Application US/09398326

Patent No. 6355863

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early

TITLE OF INVENTION: Reproductive Development and Methods of Making Same

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/659,188

FILING DATE: 05-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3739

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 273 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-398-326-8

Alignment Scores:

Pred. No.:	1,736-52	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	4	Gaps:	0

US-10-020-338-8 (1-593) x US-09-398-326-8 (1-273)

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QY 263 ATGGTCGCGGCAAGTCGACGTGAAGCGGATAGAGAACAGATTAATCGGACGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuYsArgIleGluAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAGCGCGGCAAGCGGCTCTGAAAGAGCGGCAAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgLysAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuGlyAsp 40
QY 383 GGGAGAGTCGCGGTCATCTCTTCTCCCAAGGCAAGCTCATAGTACGCCACGAC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuYsArgIleValThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGACCGCTACTCTTATGCTGAAAGGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
QY 503 ATTTCAGCTGAATCTGAAAGTGAGGAAATTTGTCGACGATACGAACTTAAGGCG 562
DB 81 IleSerAlaGlnSerGlnSerGlnLysArgTyrPheGlnLysArgLysLeuYsAla 100
QY 563 AAGATTGAGACCATACAAAAATGTCACAAG 592
DB 101 LysIleGlnThrIleGlnLysCysHisLys 110
```

RESULT 7

US-08-592-214A-4

Sequence 4, Application US/08592214A

Patent No. 5811536

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.

TITLE OF INVENTION: Cauliflower Floral Meristem Identify

TITLE OF INVENTION: Genes and Methods of Using Same

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,214A

LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-227-8

Alignment Scores:
Pred. No.: 1.73e-52 Length: 273
Score: 561.00 Matches: 109
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 54.47% Indels: 0
DB: 3 Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-227-8 (1-273)

QY 263 ATGGGTCGGGCGGAGGTGAGCGGATGAGCAAGATTAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGGAGCGGCTCCTGAAGAGCGGACGAGATCTCCGTCCTGTGAC 382
DB 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCAAGGCAAGCTTATGAGTACCGCCAGC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuTyrgIuTyraIaThrAsp 60
QY 443 TCACAGATGACAAATTTCTGAAGCTTATGAGCGGCTTATGCTGAAGAGGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgTyrgIuArgTyserTyraIaGlnLysAlaLeu 80
QY 503 ATTGAGCTGAATCTGAAGTGAAGGGAATGTGTCACGAATACAGAACTTAAGCGC 562
DB 81 IleSerAlaGlnSerGlnSerGlnLysArgTyrgIuArgTyserTyraIaGlnLysAlaLeu 100
QY 563 AAGATTGAGACCATACAAATGTGCACAG 592
DB 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 4

US-08-655-241-8
Sequence 8, Application US/08655241
Patent No. 6025543

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-241-8

Alignment Scores:
Pred. No.: 1.73e-52 Length: 273
Score: 561.00 Matches: 109
Percent Similarity: 99.09% Conservative: 0
Best Local Similarity: 99.09% Mismatches: 1
Query Match: 54.47% Indels: 0
DB: 3 Gaps: 0

US-10-020-338-8 (1-593) x US-08-655-241-8 (1-273)

QY 263 ATGGGTCGGGCGGAGGTGAGCGGATGAGCAAGATTAATCGGAGGTGACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnAsnLysIleAsnArgGlnValThr 20
QY 323 TTCTCCAAAGCGCGGAGCGGCTCCTGAAGAGCGGACGAGATCTCCGTCCTGTGAC 382
DB 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCAAGGCAAGCTTATGAGTACCGCCAGC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuTyrgIuTyraIaThrAsp 60
QY 443 TCACAGATGACAAATTTCTGAAGCTTATGAGCGGCTTATGCTGAAGAGGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgTyrgIuArgTyserTyraIaGlnLysAlaLeu 80
QY 503 ATTGAGCTGAATCTGAAGTGAAGGGAATGTGTCACGAATACAGAACTTAAGCGC 562
DB 81 IleSerAlaGlnSerGlnSerGlnLysArgTyrgIuArgTyserTyraIaGlnLysAlaLeu 100
QY 563 AAGATTGAGACCATACAAATGTGCACAG 592
DB 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 5

US-09-149-976-8
Sequence 8, Application US/09149976
Patent No. 6127123

GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,976
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,214
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-592-214A-8

Alignment Scores:

Pred. No.:	1,73e-52	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	2	Gaps:	0

US-10-020-338-8 (1-593) x US-08-592-214A-8 (1-273)

QY 263 ATGGGTCGGCGGAGGTGCACTGAACCGGATAGAGAACAGTAATTCGGCAGGTACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnAsnLysIleAsnArgIleValThr 20
QY 323 TTCTCCAGCGCGGCGGAGGCTCCTGAAGAGGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCGCAAGGCAAGCTCTATGATGACGCCAGC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuLysArgIleValThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
QY 503 ATTTGAGCTGATCTGAAGAGTGAAGGAAATTTGGTGCACGAAATACGAAACTTAAGGCG 562
DB 81 IleSerAlaGlnSerGlnSerGlnLysArgIleValThrPheValGlnLysAlaLeu 100
QY 563 AAGATTGAGACCATACAAATGTCAAG 592
DB 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 2

US-08-659-188-8
Sequence 8, Application US/08659188
Patent No. 6002069

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-188-8

Alignment Scores:

Pred. No.:	1,73e-52	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	3	Gaps:	0

US-10-020-338-8 (1-593) x US-08-659-188-8 (1-273)

QY 263 ATGGGTCGGCGGAGGTGCACTGAACCGGATAGAGAACAGTAATTCGGCAGGTACC 322
DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGlnAsnLysIleAsnArgIleValThr 20
QY 323 TTCTCCAGCGCGGCGGAGGCTCCTGAAGAGGCGCAGAGATCTCCGCTCTGTGAC 382
DB 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGlnIleSerValLeuLysAsp 40
QY 383 GCGAGGTGCGCGTCATGCTCTTCTCCCGCAAGGCAAGCTCTATGATGACGCCAGC 442
DB 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuLysArgIleValThrAsp 60
QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGCTCTT 502
DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
QY 503 ATTTGAGCTGATCTGAAGAGTGAAGGAAATTTGGTGCACGAAATACGAAACTTAAGGCG 562
DB 81 IleSerAlaGlnSerGlnSerGlnLysArgIleValThrPheValGlnLysAlaLeu 100
QY 563 AAGATTGAGACCATACAAATGTCAAG 592
DB 101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 3

US-08-655-227-8
Sequence 8, Application US/08655227
Patent No. 6025483

GENERAL INFORMATION:

APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cauliflower APETALAI Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
FILING DATE: 05-JUN-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Run on: June 24, 2003, 14:08:24 ; Search time 13.5 Seconds
(without alignments)
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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Total number of hits satisfying chosen parameters: 525148

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-FAPEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

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6: /cg2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	561	54.5	273	3	US-08-659-188-8
3	561	54.5	273	3	US-08-655-227-8
4	561	54.5	273	3	US-08-655-241-8
5	561	54.5	273	3	US-09-149-976-8
6	561	54.5	273	4	US-09-398-326-8
7	428	41.6	253	2	US-08-592-214A-4
8	428	41.6	253	3	US-08-659-188-4
9	428	41.6	253	3	US-08-655-227-4
10	428	41.6	253	3	US-08-655-241-4
11	428	41.6	253	3	US-09-149-976-4
12	428	41.6	253	4	US-09-398-326-4

13	424	41.2	255	2	US-08-576-156-2	Sequence 2, Appl1
14	424	41.2	256	3	US-08-659-188-2	Sequence 2, Appl1
15	424	41.2	256	3	US-08-655-227-2	Sequence 2, Appl1
16	424	41.2	256	3	US-08-655-241-2	Sequence 2, Appl1
17	424	41.2	256	4	US-09-398-326-2	Sequence 2, Appl1
18	424	41.2	300	2	US-08-592-214A-2	Sequence 2, Appl1
19	424	41.2	300	3	US-09-149-976-2	Sequence 2, Appl1
20	422	41.0	255	2	US-08-592-214A-6	Sequence 6, Appl1
21	422	41.0	255	3	US-08-659-188-6	Sequence 6, Appl1
22	422	41.0	255	3	US-08-655-227-6	Sequence 6, Appl1
23	422	41.0	255	3	US-08-655-241-6	Sequence 6, Appl1
24	422	41.0	255	3	US-09-149-976-6	Sequence 6, Appl1
25	422	41.0	255	4	US-09-398-326-6	Sequence 6, Appl1
26	399	38.7	242	4	US-09-067-800-2	Sequence 2, Appl1
27	399	38.7	242	4	US-09-105-652-2	Sequence 2, Appl1
28	399	38.7	242	4	US-09-349-677-2	Sequence 2, Appl1
29	392	38.1	255	2	US-08-592-214A-10	Sequence 10, Appl1
30	392	38.1	255	3	US-08-659-188-10	Sequence 10, Appl1
31	392	38.1	255	3	US-08-655-227-10	Sequence 10, Appl1
32	392	38.1	255	3	US-08-655-241-10	Sequence 10, Appl1
33	392	38.1	255	3	US-09-149-976-10	Sequence 10, Appl1
34	392	38.1	255	4	US-09-398-326-10	Sequence 10, Appl1
35	386	37.5	150	2	US-08-592-214A-14	Sequence 14, Appl1
36	386	37.5	150	3	US-08-659-188-14	Sequence 14, Appl1
37	386	37.5	150	3	US-08-655-227-14	Sequence 14, Appl1
38	386	37.5	150	3	US-08-655-241-14	Sequence 14, Appl1
39	386	37.5	150	3	US-09-149-976-14	Sequence 14, Appl1
40	386	37.5	150	4	US-09-398-326-14	Sequence 14, Appl1
41	382	37.1	251	2	US-08-592-214A-12	Sequence 12, Appl1
42	382	37.1	251	3	US-08-659-188-12	Sequence 12, Appl1
43	382	37.1	251	3	US-08-655-227-12	Sequence 12, Appl1
44	382	37.1	251	3	US-08-655-241-12	Sequence 12, Appl1
45	382	37.1	251	3	US-09-149-976-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1
US-08-592-214A-8
Sequence 8, Application US/08592214A
Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Yanoofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
NUMBER OF INVENTIONS: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
TYPE: amino acid

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Alignment Scores:
 Pred. No.: 1,45e-36 Length: 253
 Score: 428.00 Matches: 82
 Percent Similarity: 89.72% Conservative: 14
 Best Local Similarity: 76.64% Mismatches: 11
 Query Match: 41.55% Indels: 0
 DB: 18 Gaps: 0

US-10-020-338-8 (1-593) x AAW23812 (1-253)

QY 263 ATGGGTGCGGCGGCAAGGTGAGCGGATAGAGCAAGATAATGCGCAGGTGACC 322
 DB 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysIleAsnArgGlnValThr 20
 QY 323 TTCTCCAGCGCGCGCAACGGGCTCCTGAAGAGCGCAGAGATCTCCGTCTGTGAC 382
 DB 21 PheSerLysArgArgArgAlaGlyLeuMetLysLysAlaHisGlnIleSerValLeuGlyAsp 40
 QY 383 GCGGAGGTGCGCGTCATGCTCTTCTCCCGCAAGGCAAGCTCTATAGTACGCCACCGAC 442
 DB 41 AlaGlnValAlaLeuValValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
 QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTATGCTGAAGAGCTCTT 502
 DB 61 SerCysMetGlnLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnArgGlnLeu 80
 QY 503 ATTTCAGCTGAATCTGAAGAGTGAGGAAATTTGGTGCACAGATACAGAACTTAAGCGC 562
 DB 81 IleAlaProGlnSerAspSerAsnThrAsnTrpSerMetGlnTyrAsnArgLeuLysAla 100
 QY 563 AAGATTGAGACCATACAAAA 583
 DB 101 LysIleGlnLeuLeuGlnArg 107

RESULT 15

AAW69329

ID AAW69329 standard; Protein; 253 AA.

XX AAW69329;

DT 19-NOV-1998 (first entry)

DE Brassica oleracea API protein.

KW CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;

XX early flowering promotion; angiosperm; API gene.

OS Brassica oleracea.

US5811536-A.

PD 22-SEP-1998.

PF 26-JAN-1996; 96US-0592214.

PR 26-JAN-1996; 96US-0592214.

PA (REGC) UNIV CALIFORNIA.

PI Yanofsky ME;

DR WPI; 1998-530945/45.

DR N-PSDB; AAV58316.

PT Cloned CAULIFLOWER genes - and vectors for converting shoot
 PT meristems to floral meristems

PS Disclosure; Fig 2; 93pp; English.

CC This sequence is the Brassica oleracea API protein. This sequence
 CC was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER
 CC (CAL) protein of the invention. An expression vector containing the CAL
 CC DNA sequence can be used to convert shoot meristems to floral meristems.

CC especially to promote early flowering in angiosperms.
 XX SQ Sequence 253 AA;

Alignment Scores:
 Pred. No.: 1,45e-36 Length: 253
 Score: 428.00 Matches: 82
 Percent Similarity: 89.72% Conservative: 14
 Best Local Similarity: 76.64% Mismatches: 11
 Query Match: 41.55% Indels: 0
 DB: 19 Gaps: 0

US-10-020-338-8 (1-593) x AAW69329 (1-253)

QY 263 ATGGGTGCGGCGGCAAGGTGAGCGGATAGAGCAAGATAATGCGCAGGTGACC 322
 DB 1 MetGlyArgGlyArgValGlnLeuLysArgGlnLeuLysIleAsnArgGlnValThr 20
 QY 323 TTCTCCAGCGCGCGCAACGGGCTCCTGAAGAGCGCAGAGATCTCCGTCTGTGAC 382
 DB 21 PheSerLysArgArgArgAlaGlyLeuMetLysLysAlaHisGlnIleSerValLeuGlyAsp 40
 QY 383 GCGGAGGTGCGCGTCATGCTCTTCTCCCGCAAGGCAAGCTCTATAGTACGCCACCGAC 442
 DB 41 AlaGlnValAlaLeuValValPheSerHisLysGlyLysLeuPheGlnLysSerThrAsp 60
 QY 443 TCCAGCATGACAAATTTCTTGAACGTTATGAGCGCTACTCTATGCTGAAGAGCTCTT 502
 DB 61 SerCysMetGlnLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnArgGlnLeu 80
 QY 503 ATTTCAGCTGAATCTGAAGAGTGAGGAAATTTGGTGCACAGATACAGAACTTAAGCGC 562
 DB 81 IleAlaProGlnSerAspSerAsnThrAsnTrpSerMetGlnTyrAsnArgLeuLysAla 100
 QY 563 AAGATTGAGACCATACAAAA 583
 DB 101 LysIleGlnLeuLeuGlnArg 107

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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Alignment Scores:

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Score: 2.47e-37
Percent Similarity: 435.50
Best Local Similarity: 68.218
Query Match: 54.344
DB: 42.284
Indels: 11
Gaps: 3

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US-10-020-338-8 (1-593) x AAG34120 (1-307)

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QY 140 TTAAGCTGATCCCTCCCTCCCTACCGCGCGGAGGACGACGCTCGGCTCTC 199
DB 22 LeuGlnArgHisLeuIlePhePro-----SerArgLeuPro 33
QY 200 CCACCCCGCGCG-----CCGTGCGGCGCATATGACACAAGACCGACAGCTAGATCGCA 253
DB 34 ProThrArgProHisHisCysCysAspGlnSerGlnArgValGlnArgValGln 53
QY 254 AATCAGATATGCGGTGCGGCGGACGCTGACGCTGAAGCGATATGACAAAGATTAATCGG 313
DB 54 AAlaIleGlnMetClyArgGlyProValGlnLeuArgArgIleGlnSlnsnySllleAanArg 73

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QY 314 CAGGTGACCTTCTCCAGCGCGCAACGAGCTCTGAGAAGAGCGCACAGATCTCCGTC 373
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DB 134 ArgAlaValIleuAsnProSerIleGlnuSpGlnAlaSerThrGlyAspGlnTyValArg 153
QY 554 CTTAAGCGCAAGATTGACACCATTCMAAATGTGCACAG 592
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RESULT 14
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ID AAW23812 standard; Protein; 253 AA.
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AC AAW23812;
XX
DT 11-MAY-1998 (first entry)
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DE Brassica oleracea floral meristem identity gene API product.
XX
KW Floral meristem identity gene; APERLAL; API gene;
XX flower development; transgenic plant; angiosperm.
OS Brassica oleracea.
XX
PN WO9727287-A1.
XX
PD 31-JUL-1997.
XX
XX 26-JAN-1996; 96WO-US01041.
PF 26-JAN-1996; 96WO-US01041.
PR 26-JAN-1996; 96WO-US01041.
XX
PA (REGC) UNIV CALIFORNIA.
XX
XX Yanofsky MF;
PI
PI
DR WPI; 1997-393675/36.
DR N-PSDB; AAT76886 and AAT76893.
XX
PT Cauliflower floral meristem identity genes and related proteins -
PT used to develop products for converting shoot meristem to floral
PT meristem and promoting early flowering in an angiosperm
XX
XX
PS Disclosure: Fig 2A-B; 132pp; English.

This sequence comprises the Brassica oleracea APERLAL (API) gene product that is involved in the conversion of shoot meristem to floral meristem. B. oleracea API cDNA and genomic DNA sequences are provided (see AAT76886 and AAT76893). Mutation of the API gene results in replacement of a few basal flowers by inflorescence shoots that are not subtended by flowers. When API is ectopically expressed in shoot meristem, the shoot meristem is converted to floral meristem and early flowering can occur. The invention relates to floral meristem identity genes API, LFY and especially CAL (see AAT76885-97 and AAT99437) and their gene products (see AAW23811-18), and their use in converting shoot meristem to floral meristem and in promoting early flowering in transgenic plants, especially angiosperms such as cereal plants, leguminous plants, oilseed plants, trees, fruit-bearing plants or ornamental flowers.

Sequence 253 AA;

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

OS Zea mays subsp. mays.

XX EPI033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 05-MAY-1999; 99US-0132484.

PR 06-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132863.

PR 11-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135153.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 23-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0143927.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 19-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144331.

PR 19-JUL-1999; 99US-0144332.

PR 19-JUL-1999; 99US-0144333.

PR 19-JUL-1999; 99US-0144334.

PR 20-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 23-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 28-JUL-1999; 99US-0145919.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 05-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.

PR 09-AUG-1999; 99US-0147935.

PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.

PR 13-AUG-1999; 99US-0148565.

PR 13-AUG-1999; 99US-0148684.

PR 16-AUG-1999; 99US-0149368.

PR 17-AUG-1999; 99US-0149175.

PR 18-AUG-1999; 99US-0149426.

PR 20-AUG-1999; 99US-0149722.

PR 20-AUG-1999; 99US-0149723.

PR 20-AUG-1999; 99US-0149929.

PR 23-AUG-1999; 99US-0149902.

PR 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.

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PR 27-AUG-1999; 99US-0151066.

PR 27-AUG-1999; 99US-0151080.

PR 30-AUG-1999; 99US-0151303.

PR 31-AUG-1999; 99US-0151438.

PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
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 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
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 PR 18-JUN-1999; 99US-0139763.
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 PR 30-JUN-1999; 99US-0141287.
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 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142877.
 PR 13-JUL-1999; 99US-0143342.
 PR 14-JUL-1999; 99US-0143624.
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 PR 20-JUL-1999; 99US-0144632.
 PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.
 PR 21-JUL-1999; 99US-0145086.
 PR 21-JUL-1999; 99US-0145087.
 PR 22-JUL-1999; 99US-0145085.
 PR 22-JUL-1999; 99US-0145087.
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 PR 22-JUL-1999; 99US-0145192.
 PR 23-JUL-1999; 99US-0145145.
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 PR 27-JUL-1999; 99US-0145913.
 PR 27-JUL-1999; 99US-0145918.
 PR 27-JUL-1999; 99US-0145919.
 PR 28-JUL-1999; 99US-0145951.
 PR 02-AUG-1999; 99US-0146386.
 PR 02-AUG-1999; 99US-0146388.
 PR 02-AUG-1999; 99US-0146389.
 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
 PR 04-AUG-1999; 99US-0147302.
 PR 05-AUG-1999; 99US-0147192.
 PR 05-AUG-1999; 99US-0147260.
 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
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 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
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 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
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 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151067.
 PR 30-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.

Pred. No.: 1,23e-50 Length: 273
 Score: 561.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 21 Gaps: 0

US-10-020-338-8 (1-593) x AAF78883 (1-273)

QY 263 ATGGGTCCGGCGAGGTGAGCGATGAGCAACAGATTAATCGCAGGTGACC 322
 1 MetGlyArgGlyLysValGlnLeuYsArgIleGlnAsnLysIleAsnArgGlnValThr 20
 Db 323 TTCTCCAAAGCCCGCAGCGGCTCCTGAAGAGCGCAGAGATCTCCGTCCTGTGAC 382
 21 PheSerLysArgArgAsnGlyLeuLeuYsLysAlaHisGlnIleSerValLeuYsAsp 40
 QY 383 GCGAGGTCCGCGTCATGCTCTTCCGCCAAAGCGCAGCTTATGAGTACGCCACCGAC 442
 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuYsGlnIlyrAlaThrAsp 60
 Db 443 TCCAGCATGACAAATCTTGAACGTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT 502
 61 SerArgMetAspLysIleLeuGlnArgIlyrGlnArgIlyrSerTyraGlnLysAlaLeu 80
 QY 503 ATTTAGCTGAATCTGAAGAGTGAAGGAAATGGTCCACGAATACAGAACTTAAAGCGC 562
 81 IleSerAlaGlnSerGlnSerGlnYsAsnTrpCysHisGlnIlyrArgLysLeuYsAla 100
 QY 563 AAGATTGAGACCATCAAAATGTCACAG 592
 101 LysIleGlnThrIleGlnLysCysHisLys 110
 Db

RESULT 10

AAB73250
 ID AAB73250 standard; Protein; 267 AA.

AC AAB73250;

DT 14-MAY-2001 (first entry)

DE Rice MADS box protein.

KW Rice; MADS box; plant branching regulation; agriculture.

OS Oryza sativa.

XX WO200114559-A1.

PD 01-MAR-2001.

PF 18-AUG-2000; 2000WO-JP05537.

PR 19-AUG-1999; 99JP-0232318.

PA (TSUB) KUMIAI CHEM IND CO LTD.

PI (KOJI/) KOJIMA M.

PI Kojima M, Sasaki T, Nozue M, Shioiri H;

DR WPI; 2001-191647/19.

DR N-PSDB; AAF75749.

PT Rice MADS box gene for regulating plant branching to provide ornamental

PT or agricultural plants with value-added properties or increase in yield

PS Claim 2; Page 19; 43pp; Japanese.

CC The present sequence is the rice MADS box protein. The MADS box gene can

CC be used for regulating plant branching to provide ornamental or

CC agricultural plants. In addition, plants with value-added properties or

CC an increased yield can be produced using the MADS box gene.

XX SQ Sequence 267 AA;

Alignment Scores:

Pred. No.: 3.23e-50 Length: 267
 Score: 557.00 Matches: 108
 Percent Similarity: 98.18% Conservative: 0
 Best Local Similarity: 98.18% Mismatches: 2
 Query Match: 54.08% Indels: 0
 DB: 22 Gaps: 0

US-10-020-338-8 (1-593) x AAB73250 (1-267)

QY 263 ATGGGTCCGGCGAGGTGAGCGATGAGCAACAGATTAATCGCAGGTGACC 322
 1 MetGlyArgGlyLysValGlnLeuYsArgIleGlnAsnLysIleAsnArgGlnValThr 20
 Db 323 TTCTCCAAAGCCCGCAGCGGCTCCTGAAGAGCGCAGAGATCTCCGTCCTGTGAC 382
 21 PheSerLysArgArgAsnGlyLeuLeuYsLysAlaHisGlnIleSerValLeuYsAsp 40
 QY 383 GCGAGGTCCGCGTCATGCTCTTCCGCCAAAGCGCAGCTTATGAGTACGCCACCGAC 442
 41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuYsGlnIlyrAlaThrAsp 60
 Db 443 TCCAGCATGACAAATCTTGAACGTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT 502
 61 SerArgMetAspLysIleLeuGlnArgIlyrGlnArgIlyrSerTyraGlnLysAlaLeu 80
 QY 503 ATTTAGCTGAATCTGAAGAGTGAAGGAAATGGTCCACGAATACAGAACTTAAAGCGC 562
 81 IleSerAlaGlnSerGlnSerGlnYsAsnTrpCysHisGlnIlyrArgLysLeuYsAla 100
 QY 563 AAGATTGAGACCATCAAAATGTCACAG 592
 101 LysIleGlnThrIleGlnLysCysHisLys 110
 Db

RESULT 11

AAG33291
 ID AAG33291 standard; Protein; 142 AA.

AC AAG33291;

DT 18-OCT-2000 (first entry)

DE Zea mays protein fragment SEQ ID NO: 40314.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence; corn.

XX Zea mays subsp. mays.

PN EP103405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0128645.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 23-APR-1999; 99US-0130891.

Db 61 SerArgMetAspLysIleLeuGluArgTyrSerTyrIleGluLysAlaLeu 80
 QY 503 ATTTGCGTGAATCTGAAGTGGAGGAATGGTGCACGAATACAGAACTTAAGGCG 562
 Db 81 IleserAlaGluSerGluSerGluGlnGlyAsnTrpCysHisGluTyrArgLysLeuYsAla 100
 QY 563 AAGATTGAGACCATACAAATAATGTCAAG 592
 Db 101 LysIleGluThrIleGlnLysCysHisLys 110
 RESULT 8
 AA67553
 ID AAY67553 standard; Protein; 273 AA.
 XX
 AC AAY67553;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 SE Zea mays ZAPI protein.
 KM Seed plant; floral meristem; mutation; TFL gene; CAL;
 reproduction; plant breeding; API protein.
 OS Zea mays.
 XX
 PN US6025543-A.
 XX
 PD 15-FEB-2000.
 XX
 PF 05-JUN-1996; 96US-0655241.
 XX
 PR 05-JUN-1996; 96US-0655241.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Yanofsky MF;
 XX
 DR WPI: 2000-181843/16.
 DR N-PSDB; AA257057.
 XX
 PT New transgenic seed plant exhibiting early reproductive development
 PT comprises a CAULIFLOWER encoding nucleic acid and a non-mutant
 PT endogenous TERMINAL FLOWER gene -
 XX
 PS Claim 15; Columns 59-64; 51pp; English.
 XX
 CC The invention relates to a new non-naturally occurring seed plant that
 CC comprises a first ectopically expressible nucleic acid molecule encoding
 CC a floral meristem identity gene product, provided that the seed plant
 CC does not contain a mutation in an endogenous TERMINAL FLOWER (TFL) gene.
 CC that results in ectopic expression of CAL. The non-naturally occurring
 CC seed plant exhibits early reproductive development. The method of
 CC promoting early reproductive development can make breeding of long
 CC generation seed plants such as trees practical. The method can be used to
 CC increase floral meristem identity gene product expression in different
 CC crop fields at different times, resulting in a staggered time of harvest
 CC for the different fields. The present sequence represents a Zea mays
 CC API protein.
 XX
 SQ Sequence 273 AA;
 Alignment Scores:
 Pred. No.: 1,236-50 Length: 273
 Score: 561.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 21 Gaps: 0
 US-10-020-338-8 (1-593) x AAY67553 (1-273)
 QY 263 ATGGGTCCGGCAGAGGTGAGTGAAGCGAGTAGAGACAGATTAATCGCGAGGTGACC 322

Db 1 MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 QY 323 TTCTCCAAACCGCGCGAAGCGGCTCTGAAGAAAGCGCACAGATCTCCGCTCTGTGAC 382
 Db 21 PheSerLysArgArgAsnGlyLeuLeuLysAlaHisGlnIleSerValLeuGlyAsp 40
 QY 383 GCGAGGTCCGCCGTCATCGTCTTCTCCCAAGGCAAGCTTATAGTACGCCACCGAC 442
 Db 41 AlaGluValAlaValIleValPheSerProLysGlyLysLeuTyrGluTyrAlaThrAsp 60
 QY 443 TCCAGCATGGACAAATTTCTTAACGTATAGCGCTACTCTTATGCTGAAAAGCTCTT 502
 Db 61 SerArgMetAspLysIleLeuGlnArgTyrGluArgTyrSerTyrIleGluLysAlaLeu 80
 QY 503 ATTTGCGTGAATCTGAAGTGGAGGAATGGTGCACGAATACAGAACTTAAGGCG 562
 Db 81 IleserAlaGluSerGluSerGluGlnGlyAsnTrpCysHisGluTyrArgLysLeuYsAla 100
 QY 563 AAGATTGAGACCATACAAATAATGTCAAG 592
 Db 101 LysIleGluThrIleGlnLysCysHisLys 110
 RESULT 9
 AAY78883
 ID AAY78883 standard; Protein; 273 AA.
 XX
 AC AAY78883;
 XX
 DT 19-MAY-2000 (first entry)
 XX
 DE Corn APEPALAI (API) amino acid sequence.
 XX
 KM APEPALAI; API; floral meristem identity; early reproductive development;
 KM transgenic plant; selective breeding programme; disease resistance; corn.
 OS Zea mays.
 XX
 PN US6025483-A.
 XX
 PD 15-FEB-2000.
 XX
 PF 05-JUN-1996; 96US-0655227.
 XX
 PR 05-JUN-1996; 96US-0655227.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Yanofsky MF;
 XX
 DR WPI: 2000-181839/16.
 DR N-PSDB; AA92144.
 XX
 PT Purified nucleic acids encoding APEPALAI 1 (API) proteins, promote early
 PT reproductive development in seed plants, useful for accelerating
 PT selective breeding programmes -
 XX
 PS Claim 1; Column 63-64; 50pp; English.
 XX
 CC This sequence represents the APEPALAI (API) amino acid sequence from
 CC corn. API is a floral meristem identity product, that promotes conversion
 CC of shoot meristem to floral meristem in an angiosperm. Vectors containing
 CC the API gene can be used to create transgenic plants. API nucleotide
 CC sequences can be used to promote early reproductive development in seed
 CC plants which is useful for accelerating selective breeding programmes
 CC that require several rounds of crossing to produce plants with disease
 CC and insect resistance. The nucleotide sequences are particularly useful
 CC for promoting early reproductive development in long generation seed
 CC plants such as trees.
 XX
 SQ Sequence 273 AA;
 Alignment Scores:
 Pred. No.: 1,236-50 Length: 273
 Score: 561.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 21 Gaps: 0
 US-10-020-338-8 (1-593) x AAY78883 (1-273)
 QY 263 ATGGGTCCGGCAGAGGTGAGTGAAGCGAGTAGAGACAGATTAATCGCGAGGTGACC 322

OS Zea mays.
PN WO9746078-AI.
PD 11-DEC-1997.
XX
PF 05-JUN-1996; 96WO-USO9453.
PR 05-JUN-1996; 96WO-USO9453.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Yanofsky MF;
DR MPI, 1998-041770/04.
N-PStDB; AAV02763.
XX
PT Nucleic acids encoding API floral meristem identity gene product
from cauliflower and maize - useful for promoting early reproductive
development and controlling the time of seed-derived crop harvest in
e.g. grapes, beans, corn, wheat, etc

XZ Claim 1; Page 127-128; 156pp; English.

CC This protein comprises maizc floral meristem identity gene product
ZAPI, the orthologue of the Arabidopsis APETALA (AP1) gene product
(see AMW91311) that is involved in the conversion of shoot meristem
to floral meristem. Mutation of the AP1 gene results in replacement
of basal flowers by inflorescence shoots that are not subtended by
flowers. The invention relates to an expression vector comprising
a nucleic acid sequence encoding a floral meristem gene product
operably linked to a heterologous regulatory element (see
AAV02770-75). The floral meristem gene product is selected from API1,
LFY (LEAFY) and CAlL (CALFLORNER) (see AMW91311-38). The expression
vector is used to convert shoot meristem tissue to floral meristem
tissue in transgenic plants, especially angiosperms or gymnosperms,
thereby promoting early reproductive development in these plants.
This can be used to manipulate the time of crop harvest and to
hasten breeding time.

SQ Sequence 273 AA;

US-10-020-338-8 (1-593) x AAM59134 (1-273)

QY	269	ATGGGGTCGGGGCAAGGTGCAGCTGGAAGCGGATGAGAAACAATTAATCGGCAGGTGACC	3522
Db	1	MetGlyAlaGlyLysValGlnLeuLysArgGlnLeuLysLeuSerAlaGlnValThr	20
QY	323	TTCTCCACGCGCGCAACGGCGCTCTGAAGAAGCGCGACGAGATCTCCGCTCTGTGAC	3822
Db	21	PheSerLysArgArgAsnGlyLeuLysLysAlaHisGlnLysLeuValLeuCysAsp	40
QY	383	GGGAGAGTGGCGGTATCGTCTCTCCGCCCAAGGCAAGGTCTATGAGTGGCGCACCGAC	4422
Db	41	AlaGlnValAlaValIleValPheSerProlyGlyLysLeuLysGlnLysAlaThrAsp	60
QY	443	TCCAGCATGACAAATTTCTTGAACGTATAGCGGCTACTTTATGCTGAAAAGGCTCTT	5022
Db	61	SerArgMetAspLysIleLeuGlnLysGlyGlnArgLysSerLysAlaGlnLysAlaLeu	80
QY	503	ATTTCAGCTGAATCTGAAAGGTGAGGAGAAATTTGGTGCACAAATAACAGAACTTAAGGCG	5622
Db	81	IleSerAlaGlnSerGlnSerGlnLysThrProCysHisGlnLysArgLysLeuLysAla	100
QY	563	AAGATTGAGCACTACAAAATATGTACAAAG	592

Db	101	LysIleGluThrIleGlnLysCysHisIAs	110
RESULT 7			
ID	AA19244	standard; Protein; 273 AA.	
XX	AA19244;		
XX	19-FEB-2001	(first entry)	
XX	Amino acid sequence of a APETALA1 (AP1) polypeptide.		
DE	APETALA1, AP1; floral meristem identity gene; CAULIFLOWER, CAL; LEAFY;		
XX	LFY; floral meristem; early flowering.		
XX	Zea mays.		
XX	US6127123-A.		
PN	03-OCT-2000.		
XX	09-SEP-1998;	98US-0149976.	
XX	26-JAN-1996;	96US-0592214.	
XX	(REGC) UNIV CALIFORNIA.		
PA	Yanofsky MF;		
XX	WPI; 2000-618379/59.		
DR	N-PSDB; AAC61410.		
XX	Identifying a Brassica having a cauliflower phenotype involves		
PT	detecting a polymorphism associated with cauliflower locus comprising a		
PT	modified cauliflower allele that does not encode active cauliflower		
XX	gene product		
XX	Example 1; Fig 4A-B; 93pp; English.		

CC	The present sequence represents an ABEFLAL (API) polypeptide. The API
CC	polypeptide is an ectopically expressible floral meristem identity
CC	gene product. The specification also describes CAULIFLOWER (CAL) and
CC	LEAFY (LFY) gene products. CAL is involved in the conversion of shoot
CC	meristem to floral meristem. CAL is highly conserved among different
CC	angiosperms. The CAL polynucleotides may be used to shoot meristem to
xx	floral meristem, and to promote early flowering in angiosperms.
SQ	Sequence 273 AA:
Alignment Scores:	
Pred. No.:	1.23e-50 Length: 273
Score:	561.00 Matches: 109
Percent Similarity:	99.09% Conservative: 10
Best Local Similarity:	99.09% Mismatches: 1
Query Match:	54.47% Indels: 0
Ds:	21 Gaps: 0
US-10-020-338-8 (1-593) x ABAI9244 (1-273)	
QY	263 ATGGGTCCGCGCAAGTGCAGCTGACGGATAGACAACAAGATAAATCGCAGGTGACC 322
Db	1 MetGIyARgLIyLylValIGlnleuLySargILlegluWenLySIlexsnArgInValTrn 20
QY	323 TTTCACAGCGCGCGGAAGCGGCTCTGAAAGAAGGGACAGCATCTCGTCCCTGTGAC 382
Db	21 PheSerLYsARGArGAsnclyLeuenuLySLysAlahSGlnlleservalLeucyrAsp 40
QY	383 GCGAGAGTCGCCGTCATGCTTTCTCCCCCAAAGGCAGACTTGATGATGAGCGCACCGAC 442
Db	41 AlagIvalAlalavalIIleValPheSerProLySGIlyLSleuTyrcIunryrAlatrrAsp 60
QY	443 TCACAGCATGAGCAAAATTCCTTAGACGTTATGAGCGCTACTCTTATGCTGAAAAAGCTCTT 502

CC expressible nucleic acid molecule encoding a first floral meristem
CC identity gene product into the angiosperm. Ectopic expression of the
CC floral meristem gene product in the shoot meristem tissue of the
CC transgenic plant, allows selection of the time of seed development in
CC the plant which can be useful for manipulating the time of crop harvest
CC in seed-derived crops such as grapes, beans, corn, wheat, rice, hop,
CC etc., or to hasten the breeding of, e.g. tree species, for insect or
CC disease resistance.

XX Sequence 273 AA;

Alignment Scores:

Pred. No.:	1,23e-50	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	19	Gaps:	0

US-10-020-338-8 (1-593) x AAM43329 (1-273)

263 ATGGGTCCGGCGCAAGGTGAGTGAAGCGATAGAGAACAAATTAATCGGAGTGACC 322
1 MetGlyArgGlyLysValGlnLeuLysArgGlnLeuLysIleAsnArgGlnValThr 20
323 TTCTCCAGCGCGCAACGGGCTCTGAAGAGCGCAGATCTCCGCTCTGTGAC 382
21 PheSerLysArgArgGlnGlnGlnLeuLysValIleGlnIleSerValLeuGlnValThr 40
383 GGGAGGTGCGCGCGTCAATCTGCTTCTCCCAAGAGGAGGAGTCTATAGACGACGAC 442
41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuLysGlnValAlaThrAsp 60
443 TCCAGCATGACAAATTTCTGAACGTTATGAGCGCTACTCTATGCTGAAGGCTCTT 502
61 SerArgMetAspLysIleLeuGlnArgGlnValGlnValSerValIleGlnLysAlaLeu 80
503 ATTTGAGTGAATCTGAAGAGTGAAGGAGAAATGGTGCCAGCATACAGAACTTAAGGCG 562
81 IleSerAlaGlnSerGlnSerGlnGlnValAsnTrpCysHisGlnValArgLysLeuLysAla 100
563 AAGATTGAGACCATACAAATATGTCACAG 592
101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 5

AAM43329 standard; Protein; 273 AA.

AAM43329;

08-JUN-1998 (first entry)

Arabidopsis floral meristem identity gene product ZAP1.

Floral meristem identity gene; APTALAI; API; ZAP1;

transgenic plant; angiosperm; seed development; maize.

Zea mays.

WO9746079-A1.

11-DEC-1997.

04-JUN-1997; 97WO-US09682.

05-JUN-1996; 96US-0659188.

(REGC) UNIV CALIFORNIA.

Yanofsky ME;
WPI; 1998-041771/04.

DR N-PSDB; AAV06021.

XX Use of floral meristem identity genes to convert shoot meristem to
PT floral meristem - for promoting early reproductive development in
PT the plants and control timing of seed-derived crop harvest (s) in
PT e.g. grapes, beans, corn and wheat.

PS Claim 6; Page 110-112; 147pp; English.

XX This protein comprises maize floral meristem identity gene product
CC ZAP1, the orthologue of the Arabidopsis APTALAI (API) gene product
CC (see AAM43326) that is involved in the conversion of shoot meristem
CC to floral meristem. Mutation of the API gene results in replacement
CC of basal flowers by inflorescence shoots that are not subtended by
CC flowers. The invention relates to a recombinant nucleic acid that
CC comprises an inducible regulatory element (see AAV06025-28) operably
CC linked to a nucleic acid molecule (see AAV06018-24) encoding a floral
CC meristem identity gene product (see AAM43326-32), especially API,
CC CAULIFLOWER (CAL) or LEAFY (LFY). The nucleic acids are used to
CC convert shoot meristem tissue into floral meristem tissue in
CC transgenic plants, thereby promoting early reproductive development
CC in these plants. This can be useful for manipulating the time of
CC crop harvest in seed-derived crops and to hasten breeding time.

SQ Sequence 273 AA;

Alignment Scores:

Pred. No.:	1,23e-50	Length:	273
Score:	561.00	Matches:	109
Percent Similarity:	99.09%	Conservative:	0
Best Local Similarity:	99.09%	Mismatches:	1
Query Match:	54.47%	Indels:	0
DB:	19	Gaps:	0

US-10-020-338-8 (1-593) x AAM43329 (1-273)-

263 ATGGGTCCGGCGCAAGGTGAGTGAAGCGATAGAGAACAAATTAATCGGAGTGACC 322
1 MetGlyArgGlyLysValGlnLeuLysArgGlnLeuLysIleAsnArgGlnValThr 20
323 TTCTCCAGCGCGCAACGGGCTCTGAAGAGCGCAGATCTCCGCTCTGTGAC 382
21 PheSerLysArgArgGlnGlnGlnLeuLysValIleGlnIleSerValLeuGlnValThr 40
383 GGGAGGTGCGCGCGTCAATCTGCTTCTCCCAAGAGGAGGAGTCTATAGACGACGAC 442
41 AlaGlnValAlaValIleValPheSerProLysGlyLysLeuLysGlnValAlaThrAsp 60
443 TCCAGCATGACAAATTTCTGAACGTTATGAGCGCTACTCTATGCTGAAGGCTCTT 502
61 SerArgMetAspLysIleLeuGlnArgGlnValGlnValSerValIleGlnLysAlaLeu 80
503 ATTTGAGTGAATCTGAAGAGTGAAGGAGAAATGGTGCCAGCATACAGAACTTAAGGCG 562
81 IleSerAlaGlnSerGlnSerGlnGlnValAsnTrpCysHisGlnValArgLysLeuLysAla 100
563 AAGATTGAGACCATACAAATATGTCACAG 592
101 LysIleGlnThrIleGlnLysCysHisLys 110

RESULT 6

AAM39134 standard; Protein; 273 AA.

AAM39134;

08-JUN-1998 (first entry)

Maize floral meristem identity gene product APTALAI.

Floral meristem identity gene product; APTALAI; API; ZAP1;

transgenic plant; angiosperm; seed development; maize.

DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 QY 333 TTCTTCAGAGCCCGGCGAGCGGCTCCTGAAGAGCGGCGAGATCTCCGCTCTGTGAC 382
 DB 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGluIleSerValLeuLysAsp 40
 QY 333 GCGGAGGTGCGCGTATGCTCTTCCCGCAAGGCGAGCTCTATGAGAGCGGCGAGC 442
 DB 41 AlaGluValAlaValIleValPheSerProLysGlyLysLeuTyrGlnTyrAlaThrAsp 60
 QY 443 TCACGATGACCAAAATCTTGAACGTTATGAGCGGCTCTTATGCTGAAAAGCTCTT 502
 DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
 QY 503 ATTTGAGCTGAATCTGAAAGTGAAGGAAATTTGGTCCAGCATACAGAACTTAAGCGC 562
 DB 81 IleSerAlaGluSerGluSerGluLysLeuTyrGlnTyrArgLysLeuLysAla 100
 QY 563 AAGATTGAGACCATACAAAATGTCAAG 592
 DB 101 LysIleGluThrIleGlnLysCysHisLys 110

RESULT 3

AAW69328
 ID AAW69328 standard; Protein; 273 AA.

AC AAW69328;

DT 19-NOV-1998 (first entry)

DE Zea mays API protein.

KM CAULIFLOWER gene; CAL gene; shoot meristem conversion; floral meristem;
 KM early flowering promotion; angiosperm; API gene; ZAP1.

OS Zea mays.

PN US5811536-A.

PD 22-SEP-1998.

PF 26-JAN-1996; 96US-0592214.

PR 26-JAN-1996; 96US-0592214.

PA (REGC) UNIV CALIFORNIA.

XX Yanofsky MF;

DR WPI: 1998-530945/45.

DR N-PSDB; AAV58307.

PT Cloned CAULIFLOWER genes - and vectors for converting shoot
 PT meristems to floral meristems

PS Example 1; Fig 4; 93pp; English.

CC This sequence is the Zea mays API protein (ZAP1). This sequence
 CC was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER
 CC (CAL) protein of the invention. An expression vector containing the CAL
 CC DNA sequence can be used to convert shoot meristems to floral meristems,
 CC especially to promote early flowering in angiosperms.

XX Sequence 273 AA;

Alignment Scores:

Pred. No.: 1,23e-50 Length: 273
 Score: 561.00 Matches: 109
 Percent Similarity: 99.09% Conservative: 0
 Best Local Similarity: 99.09% Mismatches: 1
 Query Match: 54.47% Indels: 0
 DB: 19 Gaps: 0

US-10-020-338-8 (1-593) x AAW69328 (1-273)

QY 263 ATGGGTCCCGGCGAGGTGACCTGATGAGCGGATAGAGAAAGATTAATCGGCGAGTGAC 322
 DB 1 MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr 20
 QY 333 TTCTTCAGAGCCCGGCGAGCGGCTCCTGAAGAGCGGCGAGATCTCCGCTCTGTGAC 382
 DB 21 PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGluIleSerValLeuLysAsp 40
 QY 333 GCGGAGGTGCGCGTATGCTCTTCCCGCAAGGCGAGCTCTATGAGAGCGGCGAGC 442
 DB 41 AlaGluValAlaValIleValPheSerProLysGlyLysLeuTyrGlnTyrAlaThrAsp 60
 QY 443 TCACGATGACCAAAATCTTGAACGTTATGAGCGGCTCTTATGCTGAAAAGCTCTT 502
 DB 61 SerArgMetAspLysIleLeuGlnArgTyrGlnArgTyrSerTyrAlaGlnLysAlaLeu 80
 QY 503 ATTTGAGCTGAATCTGAAAGTGAAGGAAATTTGGTCCAGCATACAGAACTTAAGCGC 562
 DB 81 IleSerAlaGluSerGluSerGluLysLeuTyrGlnTyrArgLysLeuLysAla 100
 QY 563 AAGATTGAGACCATACAAAATGTCAAG 592
 DB 101 LysIleGluThrIleGlnLysCysHisLys 110

RESULT 4

AAW43112
 ID AAW43112 standard; Protein; 273 AA.

AC AAW43112;

DT 18-JUN-1998 (first entry)

DE APETALAI gene product from Zea mays.

KM Transgenic plant; ectopically expressed; meristem gene; APETALAI;
 KM API; CAULIFLOWER; CAL; LEAFY; LFY; reproductive development;
 KM angiosperm.

OS Zea mays.

PN WO9746077-A1.

PD 11-DEC-1997.

PF 05-JUN-1996; 96WO-US09429.

PR 05-JUN-1996; 96WO-US09429.

PA (REGC) UNIV CALIFORNIA.

XX Weigel D, Yanofsky MF;

DR WPI: 1998-041769/04.

DR N-PSDB; AAT86631.

PT Transgenic plant comprising an ectopically expressed floral meristem
 PT gene - for promoting early reproductive development and controlling
 PT the time of seed-derived crop harvest(s) in e.g. grapes, beans,
 PT corn, wheat, etc

PS Claim 12; Pages 127-128; 158pp; English.

CC The present sequence represents a floral meristem identity gene
 CC product, APETALAI (API), from Zea mays. The invention relates to
 CC a non-naturally occurring seed plant comprising a first ectopically
 CC expressible nucleic acid encoding a first floral meristem identity gene
 CC product, provided that the first nucleic acid is not ectopically
 CC expressed due to a mutation in an endogenous TERMINAL FLOWER gene.
 CC The invention describes a method of converting shoot meristem to floral
 CC meristem, especially in order to promote early reproductive development,
 CC in an angiosperm, which comprises introducing a first, ectopically

XX 25-FEB-2000; 2000EP-0301439.
 PF
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 04-MAY-1999; 99US-0132407.
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 PR 06-MAY-1999; 99US-0132485.
 PR 07-MAY-1999; 99US-0132486.
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 PR 14-MAY-1999; 99US-0134218.
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 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134841.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
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 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
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 PR 04-JUN-1999; 99US-0137502.
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 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 16-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139492.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
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 PR 24-JUN-1999; 99US-0140695.
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 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
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 PR 27-JUL-1999; 99US-0145913.
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 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
 PR 13-AUG-1999; 99US-0148565.
 PR 13-AUG-1999; 99US-0148684.
 PR 16-AUG-1999; 99US-0149368.
 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149426.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
 PR 20-AUG-1999; 99US-0149929.
 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 25-AUG-1999; 99US-0150566.
 PR 26-AUG-1999; 99US-0150884.
 PR 27-AUG-1999; 99US-0151065.
 PR 27-AUG-1999; 99US-0151066.
 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151438.
 PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
 PR 13-SEP-1999; 99US-0153758.
 PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.

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7	/SID2/gcgdata/genseq/genseqp-emb1/AA1986.DAT *
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9	/SID2/gcgdata/genseq/genseqp-emb1/AA1988.DAT *
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20	/SID2/gcgdata/genseq/genseqp-emb1/AA1999.DAT *
21	/SID2/gcgdata/genseq/genseqp-emb1/AA2000.DAT *
22	/SID2/gcgdata/genseq/genseqp-emb1/AA2001.DAT *
23	/SID2/gcgdata/genseq/genseqp-emb1/AA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	570	55.3	164	21	AAAG33290	Zea mays protein f
2	561	54.5	273	18	AAW23814	Maize floral meris
3	561	54.5	273	19	AAW69328	Zea mays AP1 prote
4	561	54.5	273	19	AAW43112	APETALA1 gene prod
5	561	54.5	273	19	AAW43329	Arabidopsis floral
6	561	54.5	273	19	AAW39134	Maize floral meris
7	561	54.5	273	21	AAAB19244	Amio acid sequenc
8	561	54.5	273	21	AAAB7553	Zea mays ZAP1 pro
9	561	54.5	273	21	AAV78883	Corn APETALA1 (AP
10	557	54.1	267	22	AAW72250	Rice MADS box prot
11	554	53.8	142	21	AAAG33291	Zea mays protein f
12	554	53.8	270	22	AAAB68357	Amio acid sequenc
13	435.5	42.3	307	21	AAAG34120	Zea mays protein f
14	428	41.6	253	18	AAW23812	Brassica oleracea
15	428	41.6	253	19	AAW69329	Brassica oleracea
16	428	41.6	253	19	AAW43110	APETALA1 gene prod
17	428	41.6	253	19	AAW39132	Brassica floral me
18	428	41.6	253	19	AAW43327	Brassica floral me
19	428	41.6	253	21	AAAB19242	Amio acid sequenc
20	428	41.6	253	21	AAV78551	B. oleracea AP1 pr
21	428	41.6	253	21	AAV78681	Brassica oleracea
22	424	41.2	255	18	AAW23811	Arabidopsis floral
23	424	41.2	255	20	AAW67571	Arabidopsis LEAFY
24	424	41.2	256	19	AAW43109	APETALA1 gene prod
25	424	41.2	256	19	AAW39131	Arabidopsis floral
26	424	41.2	256	19	AAW43326	Arabidopsis floral
27	424	41.2	256	21	AAAG17300	Arabidopsis thalia
28	424	41.2	256	21	AAAG52893	Arabidopsis thalia
29	424	41.2	256	21	AAV67550	Amio acid sequenc
30	424	41.2	256	21	AAV67550	A. thaliana AP1 pr
31	424	41.2	256	21	AAAB19241	APETALA1 (AP1) nuc
32	424	41.2	300	21	AAAB19241	Amio acid sequenc
33	424	41.2	302	19	AAW69327	Arabidopsis thalia
34	424	41.0	255	18	AAW23813	Cauliflower floral
35	422	41.0	255	19	AAW69330	Brassica oleracea
36	422	41.0	255	19	AAW43111	APETALA1 gene prod
37	422	41.0	255	19	AAW43328	Cauliflower floral
38	422	41.0	255	19	AAW39133	Cauliflower floral
39	422	41.0	255	21	AAAB19243	Amio acid sequenc
40	422	41.0	255	21	AAV78552	B. oleracea var. b
41	422	41.0	255	21	AAV78882	Cauliflower APETAL
42	420	40.8	246	20	AAW95018	Petunia MADS box t
43	413	40.1	245	17	AAW96936	Eucalyptus SOE-2L
44	413	40.1	262	21	AAV69920	MADS box protein.
45	411	39.9	244	17	AAW96934	Eucalyptus SOE-1 p